

	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	150
	CAGGCGATGA	CACTCCAGTT	GTTCGCGGTT	CAGCACTGAA	AGCGCTGGAA	200
	GGCAACCCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	GTTACCTGGA	250
	TTCTTACATC	CCAGAACCAG	AGCGTGCAAT	TGACAAGCCA	TTCCTGCTGC	300
5	CAATCGAAGA	CGTATTCTCA	ATCTCTGGTC	GTGGTACAGT	AGTAACAGGC	350
	CGTGTGAGC	GTGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	400
	TATTCAAGCG	ACTGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AACTGCTGGA	TGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	500
	GGTACTAAAC	GTGAAGAAAT	TCAACGTGGT	CAAGTACTGG	CTAAACCAGG	550
10	TTCAATCAAG	CCACACACTC	AATTCGAATC	AGAAGTATAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACCTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	700
	CGTAGAGATG	GTAATGCCAG	GCGACAACAT	CAACATGATC	GTGAC	745

15

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 830 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia rettgeri*

(B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGY	CGCCAAGTAG	GTGTWCCTTA	CATCATCGTT	100
35	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAAGTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	ATACGATTTT	CCAGGCGACG	200
	ACACTCCAGT	TGTCCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCAACCCA	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCA	GGTCACTTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTGCTG	CCAATCGAAG	350
40	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACGGTTAAA	ACAACCTTGT	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCTG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAA	550
	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCAAAAACCAG	GTTCAATCAA	600
45	GCCACACACT	AAATTCGAAT	CAGAAGTCTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACTCCATT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TCAACATGAT	CGTTACCCTG	ATCCACCCAA	800
50	TCGCGATGGA	CGACGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 151

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Providencia rustigianii*
 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
10	GTGAGCACAT	CCTGTTAGGT	CGCCAAGTAG	GTGTTTCCTTA	CATCATCGTT	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTTTCGYGGT	TCAGCACTGA	AAGCGCTGGA	AGGTATCCCT	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCC	GGTTACCTGG	ACAGCTACAT	300
15	CCCAGAACCA	GAGCGCGCAA	TTGACCGTCC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	SCGTGTTGAG	400
	CGTGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACRGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTTG	500
	ACGAAGGTCG	TGCTGGTGAG	AACGTTGGTG	TTTTACTGCG	TGGTACTAAG	550
20	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACT	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAACATGAT	CGTGACACTG	ATTCACCCAA	800
25	TCGCGATGGA	TGATGGTTTA	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 152

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia stuartii*
 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

45	CGGTGCAATC	CTAGTTGTTG	CGGCAACAGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGTGATG	200
	ACACTCCAGT	TATCCGTGGT	TCAGCGCTGA	AAGCGTTGGA	AGGCAACCCA	250
50	GAGTGGGAAG	CGAAAATCGT	TGAAGTAGCA	GAAGCACTGG	ACAGCTACAT	300
	CCCAGAGCCA	GAGCGTGCAA	TTGACAAAGCC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCAGGT	CGTGACTACG	TAGTCACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTAG	GTATCAAAGA	450
	GACTGCGAAA	ACCACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
55	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTTCTG	GCGAAACCAG	GTTCAATCAA	600
	GCCACACACA	ACTTTCGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACGCCATTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
60	GGTAATGCCA	GGCGACAACG	TGAACATGAA	AGTAACTCTG	ATTCACCCAA	800

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCCAT GCCGCAGACC CGCGAGCACA 50
 TCCTGCTGTC CCGCCAGGTA GGCGTTCCTT ACATCGTCGT GTTCCTGAAC 100
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAAGTGG TCGAGATGGA 150
 AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA 200
 25 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT 300
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350
 ACGTGTTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC 450
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGGACAACA TCAAGATGGT TGTCAACCCTG ATCGCTCCGA 800
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50
 GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT 100
 TACCTGAACA AGGCTGACCT GGTAGACGAC GCTGAGCTGC TGGAAGTGGT 150
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

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ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC 250
GACAACGAAA TGGGCACCAC GTCCGTTCGT AAACCTGGTTG AAACCTCTGGA 300
CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC 350
CAATCGAAGA CGTGTTCCTCG ATCTCCGGTC GCGGTACTGT TGTGACTGGT 400
5 CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG 450
TCTGCGTGAC ACTACCGTCA CCACCTGCAC CCGTGTGAA ATGTTCCGTA 500
AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT 550
GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG 600
TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA 650
10 AAGAAGAAGG CGGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG 700
TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCCGAAGG 750
CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA 800
TCAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T 841

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15

2) INFORMATION FOR SEQ ID NO: 155

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 841 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear
20

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(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

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  (A) ORGANISM: Pseudomonas stutzeri
  (B) STRAIN: ATCC 17588

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

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CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC 50
GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG 100
TTCCTGAACA AGGCCGACAT GGTTGATGAC GCCGAGCTGC TCGAGCTGGT 150
35 CGAGATGGAA GTTCGYGACC TGCTGTGAC CTACGACTTC CCGGGTGAYG 200
ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC 250
GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA 300
CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC 350
CGATCGAAGA CGTGTTCCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT 400
40 CGCGTAGAGC GCGGCATCGT CAAGGTTGAG GAAGAGATCG AGATCGTCCG 450
TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA 500
AGCTGCTCGA YGARGGTCTG GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT 550
GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG 600
CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGTAC GTGCTGTCCA 650
45 AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCCKAG 700
TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCCGAAGG 750
CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA 800
TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T 841

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50

2) INFORMATION FOR SEQ ID NO: 156

```

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 833 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear
55

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 (B) STRAIN: ATCC 23333

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

	GCTATTCTAG	TAGTATCAGC	AACTGACGGT	CCAATGCCAC	AAACACGTGA	50
	GCACATTCTA	TTATCACGTC	AGGTTGGTGT	ACCATACATC	ATCGTATTCA	100
10	TGAACAAATG	TGACATGGTA	GATGACGAAG	AGTTACTAGA	GCTAGTAGAA	150
	ATGGAAGTGC	GTGAATTACT	TTCAGACTAC	GACTTCCCAG	GTGATGACAC	200
	TCCAATCATC	AAAGGTTTCAG	CTTTAGAAGC	GTTAAATGGT	AACGACGGTA	250
	AGTACGGTGA	GCCAGCAGTT	ATCGAACTAC	TAAACACTCT	AGACACTTAC	300
	ATTCCAGAGC	CAGAGCGTGA	CATCGATAAG	CCATTCCCTAA	TGCCAATCGA	350
15	AGACGTATTG	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGCCGTGTTG	400
	AATCTGGTAT	CATCAAAGTT	GGTGACGAAA	TCGAAATCGT	TGGTATCAAA	450
	GACACAGTTA	AAACAACCTG	TACTGGTATC	GAGATGTTCC	GTAAGTTACT	500
	AGACGAAGGT	CGTGCTGGTG	AGAACTGTGG	TGTACTATTA	CGTGGTACTA	550
	AGCGTGAAGA	CGTACAACGT	GGTCAAGTAC	TTGCTAAGCC	AGGTTCAATC	600
20	ACTCCACACA	CCAACCTTCGA	CGCAGAAGTA	TACGTACTAT	CAAAAGAAGA	650
	AGGTGGTTCG	CACACTCCAT	TCTTAAATGG	TTACCGTCCA	CAGTTCTACT	700
	TCCGTACTAC	TGACGTAACA	GGTGCAATCA	CGTTACAAGA	AGGTACTGAA	750
	ATGGTAATGC	CAGGCGATAA	CGTTGAGATG	AGCGTAGAGC	TAATCCACCC	800
25	AATCGCTAGG	ACAAAGGTTT	ACGTTTCGCA	ATC		833

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: ATCC 33071

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACTCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATAC	ATGATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTAGATGACG	AAGAGCTGCT	GGAACGGGTA	150
	GAAATGGAAG	TTCGCGAACT	TCTGTCTGCT	TACGAATTCC	CAGGCGACGA	200
	CATCCCGGTC	ATCAAAGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGATGCTA	250
	CTTGGGAAGC	GAAAAATCATC	GAACTGGCAG	AAGCACTGGA	CAGCTACATT	300
50	CCATTGCCAG	AGCGTGCTAT	CGATAAGCCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACAGT	GGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTGGGC	GAAGAAGTTG	AAATCGTCGG	TATCAAGGAC	450
	ACTGTTAAGT	CTACTTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCGGGCGAGA	ACGTGGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCA	AGTTTGATTG	CGAAGTGATC	ATCCTGAGCA	AAGATGAAGG	650
	TGGTTCGTAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTG	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTTATGCCTG	GTGACAACGT	GAACATGGTT	GTTACCCTGA	TCCACCCAAT	800
60	CGCGATGGAT	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 158

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

20	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG	200
	ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250
25	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT	300
	CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA	400
	CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG	500
30	ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA	550
	CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA	600
	GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG	650
	GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC	700
	CGTACTACTG ACGTGAAGT CACCATCGAA CTGCCGGAAG GCGTGGAGAT	750
35	GGTAATGCCG GGCACACA TCAAATGGT TGTACCCTG ATCCACCCGA	800
	TCGCGATGGA CGACGGTCTG CGTTTCGCAA	830

40 2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

55

60	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG	200

	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGTGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
5	CGCGGTATCA	TCAAAGTGGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GA CTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGTTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
10	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

15

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

	CCTGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATTATCGT	GTTCTGAAC	100
35	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCAA	200
	TCGTTTCGTG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
40	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAARCTGCTG	GACGAAGGCC	500
	GTGCWGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCC	GGCACCATCA	AGCCGCACAC	600
45	CAAGTTCGAA	TCTGAAGTGT	ATATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

50

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Heidelberg
(B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

10	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
15	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
20	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCCG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	YACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	TTGCCGGAAG	GCGTAGAGAT	750
25	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

45	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATCATCGT	GTTCTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACGCCGA	200
50	TCGTGCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAATGGGAA	250
	GCGAAAATCA	TGAACTGGC	TGGCTACCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAAC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CTATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
55	GTCGACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGCGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AATTCTACTT	CCGTACGACT	700
60	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

5

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCTTGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAAGCGC 400
30 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTAATTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAAGCTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGGACGA CCGTCTGCGT TTCGCAA 827

40

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCGA	200
	TCGTGCGTGG	TTCCGCTCTG	AAAGCGCTGG	AAGGCGAMGC	TGAGTGGGAA	250
	GMGAAAATCA	TCGAACTGGC	TGGCTWCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
5	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAC TGCTG	GACGAAGGCC	500
	GTGCCGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
10	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

2) INFORMATION FOR SEQ ID NO: 165

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*

30 serotype Typhi

(B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

35	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
40	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
45	ACGAAGGCCG	TGCNGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACY	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
50	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

55 2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

100

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10
 CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTGTGATGAT GAAGAGCTGC TGGAACTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG 200
 15 ACCTGCCGGT TGTTCTGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
 GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTCACCTGG ATTCCTACAT 300
 CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTTGAG 400
 CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 20 CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAATGCTGCTG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA 600
 GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 25 CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 GGTAATGCCA GGCATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA 800
 TCGCTATGGA CCAAGGC 817

30

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG 50
 TCGTCAGGTT GCGTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA 100
 TGGTTGATGA TGAAGAGCTG CTGGAAGCTG TAGAAATGGA AGTTCGTGAA 150
 50 CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCTGTG 200
 TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA 250
 TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCAGAACC AGAGCGTGCT 300
 ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG 350
 TCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG 400
 55 GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT 450
 ACTGGCGTTG AAATGTTCCG CAACTGCTG GACGAAGGCC GTGCTGGTGA 500
 GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG 550
 GTCAGGTACT GGCTAAACCA GGTTCATCA AGCCACACAC CAAGTTCGAC 600
 TCAGAAGTGT ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT 650
 60 CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAAC TACGAGGACC 700

101

GTACCATCGA ACTGCCAGAA GCGTTGAAA TGGTAATGCC AGGTGACAAC 750
 GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

5

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GCGGTTTCCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
 YTGGAACTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCGCGCTG AAAGCGCTGG 200
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 GCGGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

40

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTC CTGGCGACGA 200
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA ACGCTGGAA GGCGAAGCAG 250

	AGTGGGAAGC	TAAGATTGTA	GAAGTGGCTG	AAGCGCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
5	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
10	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTTACCCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 830 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Serratia plymuthica</i>
(B)	STRAIN: DSM 4540

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
35	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTCTGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTCCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
40	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
45	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

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GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
TCATGAACAA	ATGCGACATG	GTAGATGATG	AAGAGCTGCT	GGAAGCTGGTA	150
GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
CCGCACACCC	AGTTCGAATC	TGAAGTGTA	ATTCTGTCCA	AAGACGAAGG	650
CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

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CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
GAGTGGGAAG	CGAAAATCCT	GGAAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTCTGTGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
60	TCGTTCTGTT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250

	GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
5	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTGTCTG	GACGAAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGMCCTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
10	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGCGGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

15

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 832 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Shigella sonnei</i>
(B)	STRAIN: ATCC 29930

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
40	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GAATCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
45	GCGGYCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 716 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 13301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

```

TCTGCTGCTG ACGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA      100
10 TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC      150
TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG      200
TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT      250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC AGAACGTGAT      300
TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG      350
15 TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG      400
GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA AACAACTGTT      450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA      500
CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC GTACAACGTG      550
GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC TGAATTCAAA      600
20 GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC ACACTCCATT      650
CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAACGT      700
GTGTTGTTCA CTTACC                                     716

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2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 29247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

```

TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA      100
AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG      150
45 TAATCGCTGG TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA      200
GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC      250
AGAACGTGAT TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT      300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA      400
50 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      450
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC      500
GTACAACGTG GTC AAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC      550
TGAATTCAAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC      600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT      650
55 GACGTAACGT GTGTTGTTCA CTTACCAGAA GGTMCTGAAA TGGTAATGCC      700
TGGTGATAAC GTTGAAATG                                     719

```

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```

15 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      50
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      100
   AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      150
   ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT      200
20 CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT      250
   TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      300
   ACGTATTCTC AATCACTGGT CGTGCTACTG TTGCTACAGG CCGTGTTGAA      350
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      400
   CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG      450
25 ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT      500
   CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC      550
   ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG      600
   GTGGACGTCA CACTCCATTC TTCTC                                625

```

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 43300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```

GTTGGTGTAC CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA      50
CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA      100
50 GCGAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA      150
   TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT      200
   AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA      250
   AACCATTCAAT GATGCCAGTT GAGGACGTAT TCTCAATCAC TGGTCGTGGT      300
   ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA      350
55 AGTTGAAATC ATCGGTTTAC ATGACACATC TAAAACAAC TTTACAGGTG      400
   TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT      450
   GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT      500
   ATTAGCTGCT CCTGGTTCAA TTACACCACA TACTGAATTC AAAGCAGAAG      550
   TATACGTATT ATCAAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA      600
60 AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA CTGGTGTTGT      650

```


TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
 TGAC 704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 730 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
- (B) STRAIN: ATCC 6538

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

	GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA	50
	TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT	100
	AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG	150
25	ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT	200
	CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT	250
	TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG	300
	ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA	350
	CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA	400
30	CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG	450
	ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT	500
	CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC	550
	ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG	600
	GTGGACGTGA CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTC	650
35	CGTACTACTG ACGTAACTGG TGTGTTCAC TTACCAGAAG GTACTGAAAT	700
	GGTAATGCCT GGTGATAACG TTGAAATGAC	730

40

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 834 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
- (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55

	CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC	50
	GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA	100
	TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT	150
	AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG	200
60	ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA	250

```

GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAAC TCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
5 CCGTTTCAAA AAAACAACAG TTAGTGGTGT AGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
10 TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

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15

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Staphylococcus capitis subsp. capitis
    (B) STRAIN: ATCC 27840

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
35 TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAAC TCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
40 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
45 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCACA ATTCTATTTT 700
CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCACAAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

```

50

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 804 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macrococcus caseolyticus*
 (B) STRAIN: ATCC 13548

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

	GTATCTTAGT	AGTATCTGCT	GCTGACGGTC	CAATGCCACA	AACTCGTGAA	50
	CACATCCTTT	TATCACGTAA	CGTTGGTGTA	CCAGCATTAG	TAGTATTCTT	100
10	GAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTTGAAA	150
	TGGAAGTTCG	TGACTTATTA	TCTGAATATG	ACTTCCCTGG	TGACGATGTA	200
	CCTGTAATCG	CTGGATCTGC	TTTAAAAGCA	TTAGAAGGCG	TTGAAGAATA	250
	CGAAGACAAA	ATCATGGAAT	TAATGGACGC	AGTTGATGAG	TACATCCCAA	300
	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
15	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCA	ACTGGACGTG	TTGAGCGTGG	400
	ACAAGTTAAA	GTTGGTGAAG	AAGTTGAAAT	CATTGGTTTA	ACTGAAGAAC	450
	CAGCAAAAAC	TACAGTTACA	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CTGGAGATAA	CATCGGTGCT	TTATTACGTG	GTGTTTCTCG	550
	TGAAGACGTA	CAACGTGGAC	AAGTATTAGC	TAAACCAGGT	TCAATTACTC	600
20	CACATACTAA	ATTCAAAGCT	GAAGTTTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CACTAACTAC	CGCCCTCAGT	TCTACTTCCG	700
	TACAACTGAC	GTAACGGTG	TAGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	AGATAACATC	GAAATGAACG	TTGAATTAAT	TTCTCCAATC	800
	GCGA					804

25

2) INFORMATION FOR SEQ ID NO: 184

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
45	GTGAACATAT	CCTTTTATCA	CGTAACGTTG	GTGTTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCAGCATTA	AAGCTCTTGA	AGGCGACGCT	250
	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTTCAT	300
50	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	GCGTGTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATGCAAGA	450
	AGATTCAAGC	AAAACAACG	TTACTGGTGT	AGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCGTTATT	ACGTGGTGT	550
55	GCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTTCAAT	600
	TACACCACAC	ACAAACTTTA	AAGCGGAAGT	TTACGTTTTA	TCAAAAGATG	650
	AAGGTGGCCG	TCATACGCCA	TTCTTCAGTA	ACTATCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	AGGTGTTGTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAGAAAT	GGAAGTTGAA	CTAATTCTC	800
50	CAATCGCTAT	CGAAGACGGT	ACACGTTTCT	CT		832

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	ATCTTATTAT	50
	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	100
	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	AAGTTCGTGA	150
	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	GTAATCGCTG	200
	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	ACAAAAATC	250
25	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAATC	CAGAACGTGA	300
	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	350
	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTT	400
	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	AAACAACGTG	450
	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCTGGTG	500
30	ACAACATCGG	TGCTTTTATTA	CGTGGTGTG	CACGTGAAGA	CGTACAACGT	550
	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	CAAAATTCAA	600
	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	CACACTCCAT	650
	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	TGACGTAAC	699

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
55	TTCTTAAATA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
60	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400

CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG ~~GYATCCATGA~~ 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
 5 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCACAACT ATCGTCCACA ATTCTATTTT 700
 CGTACTACTG ACGTAACTGG TGTGTGTTAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GCGGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829
 10

2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

30 CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAA AGCTTTAGAA 200
 GCGGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
 TGACTACATT CCAACTCCAG AACGTGATTG TGACAAACCA TTCATGATGC 300
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
 CGTGTGAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
 TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
 GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
 40 TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
 AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAT TACCAGAAGG 700
 TACTG 705

45

2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 23
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

	TTTTATCACG	TAACGTTGGT	GTACCAGCAT	TAGTAGTATT	CTTAAACAAA	50
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTTG	AAATGGAAGT	100
5	ACGTGACTTA	TTATCTGAAT	ACGACTTCCC	AGGTGACGAC	GTACCTGTAA	150
	TCGCTGGTTC	AGCTTTAAAA	GCTTTAGAAG	GCGATGCTCA	ATACGAAGAA	200
	AAAATCTTAG	AATTAATGCA	AGCAGTTGAT	GATTACATTC	CAACTCCAGA	250
	ACGTGACTCT	GATAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	300
	TCACTGGTCG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGTCAAATC	350
10	AAAGTTGGTG	AAGAAGTTGA	AATTATTGGT	ATCAAAGAAA	CTTCTAAAAC	400
	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	450
	CTGGTGACAA	CATCGGTGCT	TTATTACGTG	GTGTTGCTCG	TGAAGATGTA	500
	CAACGTGGTC	AAGTATTAGC	TGCTCCAGGT	TCAATTACAC	CTCACACAAA	550
	ATTCAAAGCA	GACGTATACG	TTTTATCAAA	AGATGAAGGT	GGACGTCATA	600
15	CTCCATTCTT	CACTAACTAT	CGTCCACAAT	TCTATTTCCG	TACTACTGAC	650
	GTAAGTGGTG	TTGTTAACTT	ACCAGAAG			678

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 668 bases
	(B)	TYPE: Nucleic acid
25	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus haemolyticus</i>
	(B)	STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

35	ACCAGCATT	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
40	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC	250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
	TACAGGCCGT	GTTGAACGTG	GTCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCATT	450
45	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTC	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
	TTATCTAAAG	ACGAAGGTGG	ACGTCACACT	CCATTCTTCA	CAAACATATCG	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AAGTGGTGTT	GTAACTTAC	650
50	CAGAAGGTAC	TGAAATGG				668

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 593 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
50	(D)	TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 5 (B) STRAIN: CSG 8

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 190

	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TTGAAATGGA	50
10	AGTACGTGAC	TTATTATCTG	AATACGACTT	CCCAGGTGAC	GATGTACCTG	100
	TAATCGCTGG	TTCAGCATTA	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	150
	GAAAAAATCT	TAGAATTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACTCC	200
	AGAACGTGAT	TCTGACAAAC	CATTTCATGAT	GCCAGTTGAG	GACGTATTCT	250
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	300
15	ATCAAAGTTG	GTGAAGAAAGT	TGAAATCATT	GGTATCCATG	ACACTTCTAA	350
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	400
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTGC	TCGTGAAGAC	450
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCA	GGTTCAATCA	CACCTCACAC	500
	AAAATTTAAA	GCAGACGTAT	ACGTTTTATC	TAAAGACGAA	GGTGGACGTC	550
20	ACACTCCATT	CTTCACAAAC	TATCGTCCAC	AATTCTATTT	CCG	593

2) INFORMATION FOR SEQ ID NO: 191

25

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 30 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 191

40	CGGCGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ACGTACCTGT	AATCGCTGGT	TCAGCTTTAA	AAGCTTTAGA	AGGCGATGCT	250
45	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGATTATAT	300
	TCCAACCTCCA	GAACGTGACT	CTGATAAACC	ATTTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATTATTG	GTATCAAAGA	450
	AACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
50	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTTGCT	550
	CGTGAAGATG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACA	AAATTCAAAG	CAGACGTATA	CGTTTTATCA	AAAGATGAAG	650
	GTGGACGTCA	TACTCCATTC	TTCTCTAACT	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACGTG	TGTTGTTAAC	TTACCAGAAG	GTAAGTAAAT	750
55	GGTAATGCCT	GGTGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTC			828

60 2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

```

15  ATGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC ACGTAACGTT      50
    GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA      100
    CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG      150
    AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATTA      200
20  AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT      250
    GCAAGCAGTT GATGACTACA TTCCAACCTC AGAACGTGAT TCTGACAAAC      300
    CATTCAATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT      350
    GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT      400
    TGAAATCATC GCTTTACATG ACACCTTCTAA AACAACTGTT ACTGGTGTAG      450
25  AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT      500
    GCTTTATTAC GTGGTGTGTC TCGTGAAGAC GTACAACGTG GTCAAGTATT      550
    AGCTGCTCCT GGTTCAATTA CACCACATAC AAAATTCAAA GCGGAAGTTT      600
    ACGTTTTATC TAAAGACGAA                                620
  
```

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

```

    CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA      50
    ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGA CT TATTA TCTGAATACG      100
50  ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT      150
    TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC      200
    AGTTGATGAT TATATTCCAA TTCCAGAACG TGACTCTGAT AAACCATTCA      250
    TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT      300
    ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT      350
55  TATTGGTATC AAAGAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT      400
    TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CGGTGCTTTA      450
    TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC      500
    TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT      550
    TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT      600
60  CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAAC TTACC      650
  
```


AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT :

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GGTCGTGGTA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAACTTCT 400
 AAAACAAC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTG GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTC AAGCAGACGT ATACGTTTTC TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTTGTT AACTTACCAG AAGG 684
 35

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

55 ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

	TTATTGGTAT	CAAAGAACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCTTT	450
	ATTACGTGGT	GTTGCTCGTG	AAGATGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTC	AATTACACCT	CACACAAAAT	TCAAAGCAGA	CGTATACGTT	550
5	TTATCAAAAG	ATGAAGGTGG	ACGTCATACT	CCATTCTTCA	CTAACTATCG	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTT	GTAACTTAC	650
	CAGAAGGTAC	TGAAATGTA	ATGCCTGGCG	ACAAC		685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 611 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

	GACTTATTAT	CTGAATACGA	CTTCCCAGGT	GACGACGTAC	CTGTAATCGC	50
	TGGTTCAGCT	TAAAAGCTT	TAGAAGGCGA	TGCTCAATAC	GAAGAAAAAA	100
	TCTTAGAATT	AATGCAAGCA	GTTGATGATT	ACATTCCAAC	TCCAGAACGT	150
30	GACTCTGATA	AACCATTCAT	GATGCCAGTT	GAGGACGTAT	TCTCAATCAC	200
	TGGTCGTGGT	ACTGTTGCTA	CAGGCCGTGT	TGAACGTGGT	CAAATCAAAG	250
	TTGGTGAAGA	AGTTGAAATT	ATTGGTATCA	AAGATACTTC	TAAAACAACT	300
	GTTACTGGTG	TAGAAATGTT	CCGTAAATTA	TTAGACTACG	CTGAAGCTGG	350
	TGACAACATC	GGTGCTTTAT	TACGTGGTGT	TGCTCGTGAA	GATGTACAAC	400
35	GTGGTCAAGT	ATTAGCTGCT	CCAGGTTCAA	TCACACCTCA	CACAAAATTC	450
	AAAGCAGACG	TATATGTTTT	ATCAAAAGAT	GAAGGTGGAC	GTCATACTCC	500
	ATTCTTCACT	AACTATCGTC	CACAATTCTA	TTTCCGTACT	ACTGACGTAA	550
	CTGGTGTTGT	TAACTTACCA	GAAGGTACTG	AAATGGTAAT	GCCTGGCGAC	600
40	AACGTTGAAA	T				611

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

	CGGCGGTATC	TTAGTAGTTT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
50	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTGCCAGC	ATTAGTAGTA	100

	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGATT	TATTAAGTGA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
5	TCCAACCTCCA	GAACGTGACT	CTGACAAACC	ATTTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CGTTATTACG	TGGTGTGCT	550
10	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATTG	TTCTCAAAC	ACCGCCACA	ATTCTATTTT	700
	CGTACTACAG	ACGTAAGTGG	TGTTGTTAAC	TTACCAGAAG	GTACAGAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
15	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

2) INFORMATION FOR SEQ ID NO: 198

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
40	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
45	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	GGTGGTCGTC	650
	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

50

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG 83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

```

GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT      50
ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT      100
TCCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA      150
GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT      200
TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTCATGA      250
TGCCAGTTGA GGACGTATTC TCAATCACTG GTCGTGGTAC TGTGTGCTACA      300
GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT      350
CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT      400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCATTA      450
TTACGTGGTG TTTCACGTGA TGACGTACAA CGTGGTCAAG TTTTAGCTGC      500
TCCTGGTACT ATTACACCAC ATACAAAATT CAAAGCGGAT GTTTACGTTT      550
TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCTTCAC TAACTACCGC      600
CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAATTACC      650
AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG      700
AATTAATTTC TCCAATCGCT ATT                                723
  
```

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSsa 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

```

CGTTGGTGTT CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG      50
ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAGTTCG TGAATTATTA      100
AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCTGC      150
ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT      200
TAATGCAAGC TGTTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC      250
AAACCATTCA TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG      300
TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG      350
AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT      400
GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA      450
CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC      500
AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAA ATTCAAAGCG      550
GATGTTTACG TTTTATCTAA AGATGAAGGT GGTCTGATA CACCATCTTT      600
CACTAACTAC CGCCCACAAT TCTATTTCCG TACTACTGAC GTAATTGGTG      650
TTGTTAACTT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC      697
  
```

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCTGC ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT      300
    CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACTG TAACTGGTGT TGAAATGTTT CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTT      550
    GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTCAC      800
    CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG      500
  
```

ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	556
CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTC	700
5 CGTACTACTG	ACGTAACCTGG	CGTTGTTCAA	TTACCAGAAG	GTACTGAAAT	750
GTTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
TCGCGATTGA	AGACGGTACT	CGTTTCTCAA	C		831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC	TTAGTTGTAT	CTGCAGCTGA	TGGTCCAATG	CCACAAACTC	50
GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
TTCTTAAACA	AAGTTGATAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
30 AGAAATGGAA	GTTCTGTACT	TATTATCTGA	ATATGACTTC	CCAGGTGACG	200
ACGTACCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGACGAA	250
AAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
35 CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
CACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAGTTATTAG	500
ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
40 GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTC	700
CGTACTACTG	ACGTAACCTGG	CGTTGTTCAA	TTACCAGAAG	GTACTGAAAT	750
GTTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
TCGCGATTGA	AGACGGTACT	CGTTTCTCA			829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium longum*
(B) STRAIN: ATCC 15707

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

```

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCCGATG GCCCAGACTC      50
GCGAGCACGT GCTGCTCGCC CGTCAGGTTG GCGTTCCGAA GATCCTCGTC      100
5  GCCCTGAACA AGTGCACAT GGTGACGAT GAAGAGCTCA TCGAGCTCGT      150
   CGAAGAAGAG GTCCGCGACC TCCTCGACGA GAACGGCTTC GACCGTGACT      200
   GCCCGGTCAT CCACACCTCC GCTTACGGTG CTCTGCACGA CGACGCTCCG      250
   GACCACGAGA AGTGGGTCCA GTCCGTTAAG GACCTCATGG ACGCTGTCGA      300
   CGACTACATC CCGACCCCGG TTCACGACCT GGACAAGCCG TTCCTGATGC      350
10  CGATCGAGGA CGTCTTCACC ATCTCCGGCC GTGGTACCGT TGTCACCGGT      400
   CGTGTGAGC GTGGCCAGCT GGCCGTCAAC ACCCCGGTCG AGATCGTTGG      450
   TATCCGTCCG ACCCAGCAGA CCACCGTCAC CTCCATCGAG ACCTTCCACA      500
   AGACCATGGA CGCCTGCGAG GCTGGCGACA ACACCGGTCT GCTTCTGCGT      550
   GGTCTCGGCC GTGACGATGT CGAGCGTGGC CAGGTTGTGG CCAAGCCGGG      600
15  CTCCGTCACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA      650
   AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG      700
   TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCGAGC TGCCGGAAGG      750
   CGTCGAGATG GTTCAGCCGG GCGACCACGC TACCTTCACC GTTGAGCTGA      800
   TTCAGCCCAT CGCTATGGAG GAAGGCCTGA CCTTCGCTG      839
20

```

2) INFORMATION FOR SEQ ID NO: 205

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

```

CGGCGCGATC CTGGTGTGCT CGGCCGCTGA CGGCCCCGATG CCGCAGACCC      50
40  GTGAGCACAT CCTGCTGTCG CGCCAGGTCG GCGTGCCGTA CATCGTCGTG      100
   TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TCGAGCTGGT      150
   CGAGATGGAA GTGCGCGAAC TGCTGAGCAA GTACGAGTTC CCGGGCGACG      200
   ACACCCCGAT CATCGCCGGT TCGGCCCGCC TGGCGCTGGA AGGCGACCAG      250
   AGCGACATCG GCGTGCCGGC CATCCTGAAG CTGGTCGACG CGCTGGACAG      300
15  CTGGATTCCG GAGCCGGAGC GTGCGATCGA CAAGCCGTTT CTGATGCCGG      350
   TGGAAGACGT GTTCTCGATC TCGGGCCGCG GCACCGTGGT GACCGGTCGT      400
   ATCGAGCGCG GCGTGATCAA GGTTGGCGAC GAAATCGAAA TCGTCGGCAT      450
   CCGTCCGGTG CAGAAGACCA CCGTGACCGG CGTTGAAATG TTCCGCAAGC      500
   TGCTGGACCA GGGTCAGGCA GGCGACAACG CTGGCCTGCT GCTGCGCGGC      550
50  ACCAAGCGTG ATGACGTCGA GCGTGCCAG GTGCTGGCCA AGCCGGGCAC      600
   GATCAAGCCG CACACCAAGT TCGAAGGCGA AGTGTACGTC CTGTCGAAGG      650
   ACGAGGGCGG CCGCCACACC CCGTTCTTCA ACGGCTACCG TCCGAGTTT      700
   TACTTCCGCA CCACCGACAT CACCGGCGCC GCTGCACTGC CGGAAGGCGT      750
   CGAA      754
55

```

2) INFORMATION FOR SEQ ID NO: 206

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTG TAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTGAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
	TACAACTGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
5	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
30	CCAGTTATCC	AAGGTCAGC	TCTTAAAGCA	CTTGAAGGCG	ATGAAAAATA	250
	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	CGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
35	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
40	TACAACTGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

45 2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CACTTCCCA GGTGATGACC      200
   TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
   TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
   AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
   TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10 GGTACTGTTT GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
   TATCCAAAAA GCAGTTGTGA CTGGTGTGTA AATGTTCCGT AAACAACCTG      500
   ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCOA      550
   CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
   CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15 GTGGACGTCA TACTCCATTC TTCAACAACCT ACCGTCCACA ATTCTACTTC      700
   CGTACAACCTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
   GGTATGCCTT GGTGATAACG TTACTATCGA AGTTGAATTG ATTCACCCAA      800
   TCGCCGTAGA ACAAGGTACT AC                                822

```

20

2) INFORMATION FOR SEQ ID NO: 210

```

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 825 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:
   (A) ORGANISM: Streptococcus agalactiae
   (B) STRAIN: CDCss-1073

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

```

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA      100
40 TTCATGAACA AAGTTGACCT TGTGATGAT GAAGAATTGC TTGAATTGGT      150
   TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
   ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
   AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
   TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
45 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
   CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
   AGATATCCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTT CGTAAACAAC      500
   TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
   CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
   TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
   AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTACAC      800
   CAATCGCCGT AGAACAAGGT ACTAC                                825

```

55

2) INFORMATION FOR SEQ ID NO: 211

60 (i) SEQUENCE CHARACTERISTICS:

126

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

15	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
	TGAACACATC	CTTCTTTTAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCTTCTT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTG TAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
50	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550

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CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCACC 800
CAATCGCCGT TGAACAAGGT ACTACAT 827

```

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Streptococcus anginosus (deposited as
Streptococcus constellatus)
(B) STRAIN: ATCC 27823

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25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

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GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACCTCGTGA 50
ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCTCAG GTGATGAAAT 200
CCCAGTTATC CAAGGTTTCA CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
35 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
ATCCAAAAAG CAGTTGTTAC TGGTGTTGAA ATGTTCCGTA AACAATTGGA 500
CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT 600
CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT 800
TGCCGTAGAA CAAGGAATA C 821

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45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus cricetus
(B) STRAIN: ATCC 19642

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60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

	GCTATCCTTG	TAGTAGCTTC	TACAGACGGA	CCAATGCCAC	AAACTCGTGA	50
	ACACATCTTG	CTTTCACGCC	AAGTTGGTGT	TAAGAGCCTT	ATCGTCTTCA	100
5	TGAACAAGGT	TGACTTGGTT	GACGATGAAG	AATTGCTTGA	ATTGGTTGAA	150
	ATGGAAATCC	GTGATCTTCT	TTCAGAATAC	GATTTCCTCAG	GTGATGATAT	200
	CCCTGTTGTT	CAAGGTTTCAG	CTCTTAAAGC	CCTTGAAGGT	GATACAGCTG	250
	CCGAAGACAA	GATCATGGAA	TTGATGGACA	TCGTTGATGA	CTACATTCCA	300
	GAACCAAAAC	GTGATACTGA	TAAGCCATTG	CTTCTTCCAG	TCGAAGACGT	350
10	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	TTCAGGACGT	ATCGACCGTG	400
	GTACTGTAA	GGTCAATGAC	GAAGTTGAAA	TCGTTGGTAT	CAAGGACGAA	450
	ATCCAAAAAG	CGGTTGTTAC	CGGAGTTGAA	ATGTTCCGTA	AACAATTGGA	500
	TGAAGGTCTT	GCAGGGGATA	ACGTTGGTGT	GCTTCTTCGT	GGTATCCAAC	550
	GTGATGAAAT	CGAACGTGGT	CAAGTATTGG	CTGCACCTGG	TTCAATCCAT	600
15	CCACACACTA	AATTCAAGGG	TGAAGTTTAC	ATCCTTTCTA	AAGATGAAGG	650
	TGGACGTCAC	ACTCCATTCT	TCAACAACATA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTAACTGGT	TCAATCGAAT	TGCCAGCAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACGT	TACTATCGAC	GTTGAATTGA	TCCACCCAAT	800
20	CGCTGTTGAA	AAAGGTACTA	C			821

2) INFORMATION FOR SEQ ID NO: 215

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus cristatus*
 35 (B) STRAIN: ATCC 51100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

	TATCCTTGTA	GTAGCTTCAA	CTGACGGACC	AATGCCACAA	ACTCGTGAGC	50
40	ACATCCTTCT	TTCACGTCAG	GTTGGTGTTA	AACACCTTAT	CGTCTTTCATG	100
	AACAAGATCG	ACTTGGTTGA	TGACGAAGAA	TTGCTTGAAT	TGGTTGAAAT	150
	GGAAATCCGT	GACCTCTTGT	CAGAATACGA	CTTCCCAGGT	GACGATCTTC	200
	CAGTTATCCA	AGGTTTCAGCT	CTTAAAGCTC	TTGAAGGTGA	TACTAAGTAC	250
	GAAGACATCA	TCATGGAATT	GATGAACACT	GTTGATGAGT	ACATCCCAGA	300
45	ACCAGAACGT	GATACTGACA	AACCTCTTCT	TCTTCCAGTC	GAAGACGTAT	350
	TCTCAATCAC	TGGTCGTGGT	ACAGTTGCTT	CAGGACGTAT	CGACCGTGGT	400
	ACTGTTCTGT	TCAACGATGA	AATCGAAATC	GTTGGTATCA	AAGAAGAAAT	450
	CCAAAAGCA	GTTGTTACTG	GTGTTGAAAT	GTTCCGTAAA	CAGCTTGACG	500
	AAGGTCTTGC	AGGGGACAAC	GTAGGTGTAC	TTCTTCGTGG	TATCCAACGT	550
50	GATGAAATCG	AACGTGGTCA	AGTTATCGCT	AAACCAGGTT	CAATCAACCC	600
	ACACACTAAA	TTCAAGGGTG	AAGTTTACAT	CCTTACTAAA	GAAGAAGGTG	650
	GACGTCACAC	TCCATTCTTC	AACAACATACC	GTCCACAGTT	CTACTTCCGT	700
	ACAACCTGACG	TTACAGGTTT	AATCGAACTT	CCAGCAGGTA	CTGAAATGGT	750
	AATGCCTGGT	GATAACGTAA	CTATCGACGT	TGAGTTGATC	CACCCAATCG	800
55	CCGTTGAACA	AGGTACTCCT	T			821

2) INFORMATION FOR SEQ ID NO: 216

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

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15  AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
    TTTACGTCAC GGTGTTGGTGT AAGAACCTTA TCGTCTTCAT GAACAAGGTT      100
    GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
    TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC      200
    AAGGTTTCAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
20  ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
    TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
    CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG      400
    GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC      450
    AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
25  CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
    GAACGTGGTC AAGTGTGGC TGCGCCTGGT TCGATTCCAC CACACACTAA      600
    GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
    CTCCATTCTT TAACAACTAC CGTCCACAGT TCTACTTCCG TACAACTGAC      700
    GTAACGGTT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
30  TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792
  
```

2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

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50  GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
    CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA      100
    TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
    CGTGACCTTC TTTCAGAATA CGATTTCCTT GGTGATGACC TTCCAGTTAT      200
    CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
55  TCATCATGGA ATTGATGGAT ACTGTTGATT CATACTTCC AGAACCAGAA      300
    CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
    CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC      400
    GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
    GCTGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACCTG ACGAAGGTCT      500
50  TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAT CGTGACGAAA      550
  
```

	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTC	TTCAACAAC	ATCGTCCACA	ATTCTACTTC	CGTACAAC	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus equi* subsp. *equi*
- (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTAAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTC	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus ferus*
- (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

	CGGTGCAATC	CTTGTAGTAG	CTTCTACAGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTAG	GTGTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TGCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
5	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATACT	250
	GCTCAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACCGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ATGTATTCTC	AATCACAGGT	CGTGGTACTG	TAGCTTCAGG	ACGTATCGAT	400
	CGTGGTACTG	TAAGAGTCAA	CGATGAAGTT	GAAATCGTTG	GTATCAAAGA	450
10	CGAAATCACT	AAAGCAGTTG	TTACCGGTGT	TGAAATGTTC	CGTAAACAAT	500
	TGGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTGCTTCT	CCGTGGTGTG	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCATACACCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
15	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: ATCC 10558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTCTCA	CGCCAAGTTG	GTGTAAACA	CTTGATCGTG	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAGTTGGT	150
10	TGAAATGGAA	ATCCGTGACC	TCTTGTCAGA	ATACGACTTC	CCAGGTGACG	200
	ATCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATATGAAG	ATATCATCAT	GGAATTGATG	AACACTGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGCGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
15	CGTGGTATCG	TTAAAGTCAA	TGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
	AGAAATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCAAGG	GACAACGTTG	GTGTGCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTATATCCTT	ACTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTTAC	AGGTTCAATC	GAACCTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACT			826

55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TG	TA	GT	AG	CT	TC	AA	CT	GA	CG	GAC	CA	AT	GC	TC	AA	CT	CG	GA	AC	AT	AT	CC	50
	TT	CT	TT	CA	CG	TC	AA	GT	AG	GT	GT	TAA	AT	AC	TT	AT	TG	CT	CA	TG	AA	CA	AA	100
15	GT	TG	AC	TT	GG	TT	GA	CG	AT	GA	AGA	AT	TG	CT	GA	AT	TG	GT	AA	AT	GG	AA	AT	150
	CC	GT	GAT	CT	TT	CT	TT	CAG	AA	AT	AC	GAT	TT	CC	AG	GT	GAT	GAT	AT	TC	CAG	TAA		200
	TC	CA	AG	GT	TC	AG	CA	CT	TAAA	GCT	CT	TG	AA	GT	GAT	GAAA	AT	AT	GA	AG	AC		250	
	AT	CAT	CAT	GG	AAT	TG	AT	GAA	TAC	TG	TT	GA	GA	AT	AT	AT	TC	CAG	AA	CC	AG	AC	300	
	AC	GT	GAT	ACT	GAC	AA	AC	CA	TG	CT	TCT	TC	AG	TC	GA	AG	AT	GT	AT	TCT	CA		350	
20	TC	ACT	GG	AC	TG	GT	ACT	GT	GCT	TC	AG	GA	GT	AT	CG	AC	CG	TG	GT	ACT	GT		400	
	AA	AG	TC	AA	CG	AT	GA	AG	TT	GA	AA	TC	GT	GG	AT	CC	GC	GAG	AA	AT	CC	AA	AA	450
	AG	CAG	TT	GT	ACT	GG	TG	TT	AA	AT	TCC	G	TAA	AC	AA	TT	GAC	GA	AG	GT	C		500	
	TT	GCT	GG	AG	TA	AC	GTA	GG	GTT	CT	TCT	TC	GT	GG	TAT	CC	AC	GT	GAC	GA			550	
	ATT	GA	AC	GT	GAC	AA	GT	TCT	TG	CT	AA	AC	GG	TT	CA	AT	AT	CC	AC	AC	AC		600	
25	TAA	AT	TCAA	AA	GG	TGA	AG	TTT	AC	AT	CC	TT	TAA	AGA	AAG	AA	GG	TG	GAC	GT	C		650	
	ATA	CT	CC	ATT	CT	TCA	ACA	AC	TAC	CG	TC	CT	AA	TT	CT	ACT	CC	GT	ACT	ACA			700	
	GAC	GT	TAC	AG	GTT	CA	AT	CG	ACT	TC	CT	GCA	GG	TACT	GAAA	TG	GT	AA	TGCC			750		
	TG	GT	GATA	AC	GTA	ACA	ATT	G	AT	GT	TG	AG	TT	GAT	CC	AC	CCA	ATT	G	CC	CG	TA	799	

30

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus macacae*
 (B) STRAIN: ATCC 35911

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TG	GT	GCT	ATT	CT	TG	TAG	TAG	CT	TCA	ACT	G	CG	GT	CCA	AT	G	CT	TCA	AA	C	G	50	
	GT	GA	AC	AT	AT	CT	T	CT	TT	CA	CG	CC	AA	GT	AG	TAG	GT	GT	TAA	AAA	AA	100		
50	TT	CAT	GA	ATA	AAG	TT	G	ACT	AG	TT	G	AT	G	AT	GA	AA	TT	G	TT	GA	AA	TT	G	150
	TG	AA	AT	GG	AA	AT	CC	GT	GAT	C	TT	CT	TAC	AGA	AT	AT	G	AT	TT	C	CC	AG	G	200
	AA	CT	TCC	AG	TAT	CCA	AG	GT	TC	AG	CA	CT	TA	AA	AG	CT	CT	TGA	AG	GT	GAT	ACT		250
	AAG	TAC	GA	AG	AT	ATT	AT	CAT	GGA	ATT	G	TT	G	GAT	ACT	G	TAG	AT	G	ATT	AC	AT	300	
	CCC	AGA	AC	CA	CA	AC	GT	GATA	CT	GAC	AA	GC	ATT	G	CT	TT	CT	CC	AG	TC	GA	AG	350	
55	AT	G	TTT	TCT	TAT	TACT	GGA	CG	TGG	TACT	G	TT	G	CT	T	CAG	AC	GT	ATT	G	AC	400		
	CG	TGG	TACT	G	TTA	AGG	TTAA	TG	AT	GA	AG	TT	GAA	AT	CG	TT	G	GT	AT	TC	GT	GA	450	
	CG	AT	ATT	CAA	AA	AG	CAG	TTG	TT	ACT	GG	TG	TG	AA	AT	G	TT	CG	TAA	AC	AG	C	500	
	TT	GAC	GA	AG	TCT	TG	CT	GG	GAT	A	AC	GT	C	GT	G	TC	CT	T	TC	GT	GG	TAT	C	550
	CA	AC	GT	GAT	AA	ATT	GA	AC	CG	GT	CA	AG	TT	CT	TG	CT	AA	AC	CAG	GAT	CA	AT		600
50	TC	AT	CC	AC	AT	ACT	AA	ATT	CA	AAG	GT	GA	AG	TT	AT	AT	T	CT	ACT	AA	AG	AA	G	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as
Streptococcus mitis)
 (B) STRAIN: ATCC 33399

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACTTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: ATCC 25175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTTAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTTCT	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTC	600
	AATTCACCCA	CATACTAAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
(B) STRAIN: ATCC 15912

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	GTAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCCA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTTGTTT	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCAGTTGTGA	CTGGTGTTGA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTG	TTCAACAAC	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAACTGG	ATCTATCGAA	CTTCCACCAG	GAAGTGAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ratti*
(B) STRAIN: ATCC 19645

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAAATC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: *Streptococcus sanguinis*
(B) STRAIN: ATCC 10556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTGG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GGTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Streptococcus sobrinus*
 (B) STRAIN: ATCC 33478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

25	TGTAGTAGCT	TCTACTGACG	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
	TGCTTTCACG	CCAAGTTGGT	GTAAAGAACC	TCATCGTCTT	CATGAACAAG	100
	GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCT	AGGTGACGAC	ATTCCTGTTG	200
	TTCAAGGTTT	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
	AAGATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA	300
30	ACGCGATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
	AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
	AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
	TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
35	ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC	600
	TAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
	GACGTAAC	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
40	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

50	TGTAGTAGCT	TCAACTGACG	GTCCAATGCC	ACAAACTCGT	GAGCACATCC	50
	TTCTTTCACG	TCAGGTTGGT	GTAAACACC	TTATCGTCTT	CATGAACAAA	100

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      GTTGA CTTGG TTGACGATGA AGAATTGCTT GAGTTGGTTG AAATGGAAAT      150
      CCGTGACCTT CTTTCAGAAT ACGATTTCCC AGGTGATGAT CTTCCAGTTA      200
      TCCAAGGTTT AGCTCTTAAA GCTCTTGAAG GTGACTCTAA GTACGAAGAC      250
      ATCGTTATGG AATTGATGAA CACTGTTGAT GAGTACATTC CAGAACCAGA      300
5     ACGCGACACT GACAAACCAT TGTTGCTTCC AGTCGAGGAC GTATTCTCAA      350
      TCACTGGTCG TGGTACTGTA GCTTCAGGAC GTATCGACCG TGGTACTGTT      400
      CGTGTCAACG ACGAAATCGA AATCGTTGGT CTTCAAGAAG AAAAATCTAA      450
      AGCAGTTGTT ACTGGTGTG AAATGTTCCG TAAACAACCTT GACGAAGGTC      500
      TTGCCGGCGA TAACGTTGGT GTGCTTCTTC GTGGTGTACA ACGTGATGAA      550
10    ATCGAACGTG GTCAAGTTAT CTCTAAACCA GGTTCATCA ACCCACACAC      600
      TAAATTCAAA GGTGAAGTTT ACATCCTTAC TAAAGAAGAA GGTGGACGTC      650
      ACACTCCATT CTTGACAAC TACCGTCCAC AGTTCTACTT CCGTACAAC      700
      GACGTAACG GTTCAATCAA ATTGCCAGAA GGTACTGAAA TGGTAATGCC      750
      TGGTGATAAC GTTACTATCG ACGTTGAATT GATCCACCCA ATCGCCG      797
15

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2) INFORMATION FOR SEQ ID NO: 230

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20    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 793 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus uberis
30    (B) STRAIN: ATCC 19436

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

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      TTGTTGTTGC ATCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC      50
35    CTTCTTTTAC GCCAAGTTGG TGTTAAACAC CTTATCGTTT TCATGAACAA      100
      AATCGACCTT GTTGACGATG AAGAATTGCT TGAATTAGTT GAAATGGAAA      150
      TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA CCTACCAGTT      200
      ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
      CATCATCATG GAATTGATGA AAATGTTTGA TGAGTATATT CCAGAACCAG      300
40    AACGTGATAC AGACAAACCA TTA CTCTTCTC CAGTCGAAGA CGTATTCTCA      350
      ATCACAGGTC GTGGTACTGT AGCTTCAGGA CGTATCGATC GTGGTACTGT      400
      TCGTGTCAAC GACGAAATTG AAATCGTTGG TATCAAAGAA GAAACTAAAA      450
      AAGCAGTTGT TACTGGTGTG GAAATGTTCC GTAAACAACCT TGACGAAGGT      500
      CTTGCAGGAG ATAACGTAGG TATCCTTCTT CGTGGTGTTC AACGTGACGA      550
45    AATCGAACGT GGACAAGTTA TTGCTAAACC AGGTTCAATC AACCACACA      600
      CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGATGA AGGTGGACGT      650
      CATACTCCAT TCTTCAACAA CTACCGTCCT CAATTCTATT TCCGTACAAC      700
      TGACGTAACA GGTTCATCG AACTTCCAGC TGGTACTGAA ATGGTAATGC      750
      CTGGTGATAA CGTGACAATC AGCGTTGAGT TGATCCACCC AAT      793
50

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2) INFORMATION FOR SEQ ID NO: 231

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55    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 798 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
50

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus vestibularis*
 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

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10 TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
   CTTCTTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA      100
   AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA      150
   TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA TATTCCAGTT      200
   ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
   CATCATCATG GACTTGATGA ACACTGTTGA CGAATACATT CCAGAACCAG      300
15 AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA      350
   ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTTGT      400
   TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA      450
   AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAACT TGACGAAGGT      500
   ATTGCCGGAG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA      550
20 AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCACACA      600
   CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT      650
   CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC      700
   TGACGTAACA GGTTC AATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC      750
   CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG      798
25

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2) INFORMATION FOR SEQ ID NO: 232

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tatumella ptyseos*
 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

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45 GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
   TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
   TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA      200
   CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG      250
   AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCTTGCTGC CAATCGAAGA      350
   CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGGTAGAGC      400
   GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
55 GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA      600
   CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACCTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT      800
50 CGCGATGGAC GATGGTCTGC GTTTCGCAA      829

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2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGATGA	200
	CACGCCGATC	GTACGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
25	AGTGGGAAGC	GAAAATCATC	GAACCTGGCAG	GTTTCCTGGA	TTCTTACATT	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CAACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGAATGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55	CGGCGCTATC	TTGGTTGTAT	CCGCAGCTGA	CGGCCCTATG	CCTCAAATCTC	50
	GCGAACACAT	CTTGTTGGCT	CGCCAAGTTG	GTGTTCTCTG	AATCGTAGTA	100
	TTCTTGAACA	AAGCTGACAT	GGTTGACGAT	GAAGAATTGA	TCGAATTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTTTCTTC	CTACGAATTC	CCTGGCGACG	200
60	AAGTACCTAT	CGTTGTAGGT	TCCGCGTTGA	AAGCTTTGGA	AGGCGATGCT	250

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	ACTCCTACAT	300
	CCCAACACCA	GTTCTGTGACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTTAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTC	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGTT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

15

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTTGGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCCA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGGTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGTA CTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACCAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCTCAGTT	CTACTTCCGT	700
	ACAACTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

50

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

```

GGCGCGATCC TGGTTGTTGC TGCCACTGAT GGCCCGATGC CACAGACTCG      50
CGAGCACATT CTGTTAGGGC GTCAGGTGGG TGTTCCCTTAC ATCCTGGTCT      100
10 TCCTGAACAA ATGTGACATG GTTGACGACG AAGAGCTGCT GGAAGTGGTA      150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CTGGCGACGA      200
CACTCCAGTT ATCCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCTG      250
AGTGGGAAGC AAAAATCATC GAATTGGCTG AGGCGCTGGA TAGCTATATT      300
CCACAGCCAG AGCGTGCGAT TGATAAACCA TTCCTGCTGC CAATCGAAGA      350
15 CGTATTCTCA ATCTCTGGCC GTGGTACTGT TGTCACCGGT CGTGTAGAGC      400
GCGGTATCGT TAAAGTCGGC GAAGAAGTCG AAATCGTTGG TATCATTTGAT      450
ACCATCAAGA CTACCTGTAC TGGTGTGTA ATGTTCCGCA AATTGCTGGA      500
CGAAGGCCGT GCGGGTGAGA ACGTTGGTGT TCTGCTACGT GGTACTAAAC      550
GTGATGACGT ACAACGTGGT CAGGTATTGG CAAAACCAGG TTCTATCAAG      600
20 CCACACACCA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
TGGTCGCCAT ACTCCGTTCT TCAAAGTTA TCGTCCTCAG TTCTACTTCC      700
GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
GTGATGCCAG GTGATAACAT TCAAATGATT GTTAACCTGA TTGCTCCTAT      800
25 CGCAATGGAT GACGGTCTGC GCTTTGCG      828

```

2) INFORMATION FOR SEQ ID NO: 237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*
 (B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

```

CTTGTTGTC GCTGCAACTG ATGGTCCTAT GCCACAGACT CGCGAGCACA      50
45 TCCTGCTAGG TCGTCAGGTG GGTGTTCTT ACATCCTGGT CTTCCTGAAC      100
AAGTGTGACA TGGTTGACGA TGAGGAGTTG CTGGAATTGG TAGAAATGGA      150
AGTCCGCGAA CTTCTGTCTC AATATGATTT CCCTGGCGAT GATACTCCTG      200
TTATCCGTGG TTCAGCGCTG AAGGCGTTGG AAGGCGAGCC TGAATGGGAA      250
GCAAAAATTA TCGAATTAGC TGAGGCGCTG GATAGTTATA TTCCACAGCC      300
50 AGAGCGCGCG ATTGATAGAC CATTCTTGCT GCCAATCGAA GACGTATTCT      350
CTATCTCAGG TCGTGGTACA GTCGTCTACTG TCGTGTAGA GCGTGGGATC      400
GTTAAAGTTG GCGAAGAAGT TGAAATCGTT GGTATTATCG ATTCCATTAG      450
AACACATGT ACTGGCGTTG AAATGTTCCG CAAATTGCTG GACGAAGGCC      500
GCGCGGGTGA GAACGTTGGT GTTCTACTGC GTGGGACTAA ACGTGATGAC      550
55 GTACAGCGTG GTCAGGTATT AGCTAAGCCA GGTTCATCA AGCCACATAC      600
TAAATTCGAA TCCGAAGTTT ATATTCTGAG CAAAGATGAA GGCGGGCGTC      650
ACACGCCGTT CTTCAAAGGC TACCGTCCTC AGTTCTACTT CCGTACAACG      700
GATGTAACCG GTACTATTGA ATTGCCAGAC GGCGTTGAGA TGGTGATGCC      750
AGGTGATAAC ATTCAAATGA TTGTTAACCT GATTGCACCT ATTGCGATGG      800
50 ATGATGGTCT GCG      813

```

2) INFORMATION FOR SEQ ID NO: 238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

20	GGAGCGATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCTATGC	CGCAGACTCG	50
	TGAGCATATC	CTGCTGGGCC	GCCAGGTTGG	TGTCCCATAC	ATTATTGTCT	100
	TCCTGAACAA	ATGTGACATG	GTTGACGATG	AAGAGTTGCT	AGAGTTGGTT	150
	GAAATGGAGG	TTCGTGAGCT	TCTGTCTCAA	TACGATTTC	CAGGCGACGA	200
	CACTCCAGTC	ATCCGTGGTT	CAGCGTTGAA	AGCCCTGGAA	GGTGACGCTG	250
25	AGTGGGAAGC	TAAAATTATC	GAGTTGGCAG	AAGCTCTGGA	TAGCTATATT	300
	CCGCAACCAG	AACGCGCTAT	TGATAGACCA	TTCCTATTGC	CAATTGAAGA	350
	CGTATTCTCT	ATTTCTGGTC	GTGGTACTGT	AGTTACTGGT	CGTGTAGAAC	400
	GTGGTATTGT	TAAGGTCGGC	GAAGAAGTTG	AAATCGTTGG	TATTATCGAT	450
	ACGATTAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGCA	AGCTGCTGGA	500
30	TGAAGGCCGT	GCTGGTGAAA	ATGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGATGT	TCAGCGTGGT	CAAGTACTGG	CGAAACCAGG	TTCTATCAAG	600
	CCACACACGA	AGTTTGAGTC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	CGGCCGTCAT	ACACCGTTCT	TCAAGGGCTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATTGAGC	TGCCAGAAGG	CGTTGAAATG	750
35	GTCATGCCTG	GTGACAACGT	AAACATGGTT	GTAAACCTAA	TTGCTCCTAT	800
	CGCAATGGAT	GATGGTCTGC	GCTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

55	TGGAGCGATC	TTGGTTGTTG	CTGCAACCGA	TGGCCCTATG	CCGCAGACTC	50
	GTGAGCATAT	CCTGCTGGGC	CGCCAGGTTG	GTGTCCCATA	CATTATTGTC	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAT	GAAGAGTTGC	TAGAGTTGGT	150
	TGAAATGGAG	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
50	ACACTCCAGT	CATCCGTGGT	TCAGCGTTGA	AAGCCCTGGA	AGGTGACGCT	250

	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ĀTAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCCATTATG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGAATTAA	ACAAC TTGTA	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAAC TG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCTTA	CATCTTAGTC	100
	TTCCTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAAC TGGT	150
35	TGAAATGGAA	GTTCTGTGAG	TTCTGCTCA	ATACGATTC	CCTGGCGATG	200
	ACACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAAC TTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTTGCA			829

50

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

```

5      TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
      GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10     TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
      AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG      200
      ACACTCCGAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
      GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTTCCTGG ATTCTTACAT      300
      CCCAGAACCA GTTCGTGCTA TCGACCTGCC GTTCCTGCTG CCGATCGAAG      350
15     ACGTATTCTC CATCTCCGGT CGTGGCACCG TTGTTACCGG TCGTGTAGAG      400
      CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
      GACTGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGCTG      500
      ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
      CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GTTCCATCAA      600
20     GCCGCACACC AAATTCGAAT TGAAGTTTA TATCCTGTCC AAAGACGAAG      650
      GCGGCCGCTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
      CGTACAACCTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
      GGTAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
      TCGC
25

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2) INFORMATION FOR SEQ ID NO: 242

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*
 (B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

```

45     TCAGTTCCCC CGCGATCACA TGCCCAAGAT CTACGAAGCG CTTACTCTGG      50
      CCGACGAGGG TTCCTCGTTC GCCGAAAAGG GTCTGACGCT GGAAGTGCAG      100
      CAACAGCTGG GCGACGGCGT GGTGCGTACC ATCGCGCTGG GCTCCAGCGA      150
      CGGCCTGCGC CGCGGTATGA AGGTCACCGG TACGGGCGCG CCGATCTCGG      200
      TGCCGGTCCG CACCGGCACG CTGGGCCGCA TCATGGACGT GCTGGGTCGT      250
50     CCCATCGACG AAGCCGGCCC GATCCAGCAC GAAGAAAAGC GTGGCATTCA      300
      CCAGCCGGCT CCCC GTTTCG ACGAAGTCTC GCCGTCGGTG GAACTGCTGG      350
      AAACCGGCAT CAAGGTTATT GACCTGGTCT GCCCGTTCGC CAAGGGCGGC      400
      AAGGTCGGCC TGTTCCGGCG CGCCGGCGTG GGCAAGACCG TCAACATGAT      450
      GGAAGTATGC AACAACATCG CCAAGCAGCA CAGCGGCTTG TCGGTGTTCTG      500
55     CCGGCGTGGG CGAGCGTACC CGCGAAGGCA ACGACTTCTA CCACGAAATG      550
      GAAGAGTCGA ACGTTCTGGA CAAGGTTGCG ATGGTGTTCTG GTCAGATGAA      600
      CGAACCCCGG GGCAACCGTC TGCGCGTGGC GCTGACCGGC CTGACCATGG      650
      CCGAGAAGTT CCGCGACGAA GGCCGCGACA TCCTGTTCTT CGTGGACAAC      700
      ATCTACCGCT ACACCCTGGC CGGTACGGAA GTGTCCGCGC TGCTGGGCCG      750
60     TATGCCGTCG GCAGTGGGCT ACCAGCCAC GCTGGCCGAA GAAATGGGCA      800

```

AGCTGCAAGA GCGCATCACC TCGACCAAGA CCGGCTCGAT CACCTCGAT

849

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAAC TGGTGATGGT GTTGTTTCGTA 50
 CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100
 AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGCCCG 150
 TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
 25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
 GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
 TTGCCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCCGGT GGTGCTGGTG 350
 TTGGTAAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
 CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
 30 TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500
 CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
 GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
 AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAA ATCTACCGTT 650
 ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
 35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
 GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

10 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
 (B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AACTACATT 50
 AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
 GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
 CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
 50 TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTTCCGGTGG	TGCCGGTGTG	GGTAAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTTCG	CTGGTGTTCG	TGAGTCGTA	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTCG	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTACTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG-197

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAAG	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 851 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis*
 (B) STRAIN: ATCC 15554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

	TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
	CGAAAGTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
10	AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
	CTGCGCCGCG	GTATGGAAGT	GGCCGGTTCG	GGCGCTCCCA	TCTCCGTTCC	200
	CGTGGGTGTC	GGCACCCTGG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
	TTGACGAAGT	CGGTCCTATT	CAGTCCGACG	AGCGTCGCGC	CATTACCAG	300
	CCTGCGCCTA	CTTTCGACGA	ACTGTCGCCT	TCCGTAGAGC	TGCTGGAAAC	350
15	CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTCGCCAAG	GGTGGTAAGG	400
	TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
	CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCGG	500
	TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
	ATGCTGGCGT	TATCCAGATG	GACAACCTGA	GCGAGTCCAA	AGTGGCCATG	600
20	GTGTTCCGTC	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
	GTCCGGCCTG	ACCATGGCCG	AGAAGTTCCG	TGACGAAGGC	CGTGACATCC	700
	TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCGG	TACAGAAGTG	750
	TCCGCTCTGC	TGGGTCGTAT	GCCTTCCGCA	GTGGGTTACC	AGCCTACGCT	800
25	GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
	G					851

2) INFORMATION FOR SEQ ID NO: 247

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

15	GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
	CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
	TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
	GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCACT	200
	TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
50	ACTTAGATGG	TGAGGTTTCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
	CAAGCACCTG	CATTCTGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
	TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
55	TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
50	ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800

ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT

846

5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
 CATGAACCTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
 GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCGTGG CACAGAAGTA 150
 GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
 25 ACGTGTATTC AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAACTTC 250
 CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTCGAA 300
 GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
 CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
 30 CAAGAGCACG GTGGTATCTC TGTATTGCTG GGTGTAGGTG AGCGTACTCG 500
 TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
 AAAGTGCATG GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
 CGTGTTGCAT TAACAGGTTT AACAATGGCT GAGCATTTCC GTGATGAGCA 650
 AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
 35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
 TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
 ATCTACAAAT 810

10 2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 944 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
 CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
 CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
 50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCG	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTG	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides ovatus*
- (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAAATACTG	GTTGTAGAAG	TTGAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAAT	400
	CGGTTTGTTT	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACCTGGG	TCTTTCGAAA	GTGGATTATA	ACGAACTGGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGAATGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTCTT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*

(B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTC	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCCTGGG	CCGTATCATG	AACGTCTTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAAC	GCTGGAAACC	GGCATCAAAG	350
20	TTATCGACCT	GATGTGTCCG	TTCGCGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTAATCGTGA	GGGTAACGAC	TTCTACACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTCG	TGACGTACTG	CTGTTCGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
30	TCACCTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*

45

(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGCAGCTG	GGCGACGGCG	TGGTGCCTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGGTCG	GCGCCGGCAC	CCTGGGCGCG	ATCATGGACG	TGCTGGGCGG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACCGCGCTGC	GCCGTCGTAT	GAAGACCACT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCCGTTTC	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCCGGC	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAACCTGAT	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCCTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTCG	CCCTGACCGG	CCTGACCATG	600

	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTC	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCCGC	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

```

TTCCCGGTGG GCCACCTGCC CGACATTTAC AATGCACTTA CCGTTGAACT      50
GKCCAACACC GGYGTCCACG AASAGGGCGA GACCACCAAG AAGATCACCC      100
TTGMGGTTGA ACAGCATCTT GGCGATTCCA CCGTGCGTAC CGTCGCTCTG      150
5 AAGCCGACTG ACGGCCTTGT GCGTGGCGCC ACCGTGTATG ACACCGGCGG      200
CCCgatctct GTGCCGTTG GCGATGTCAC CAAGGGCCAC GTATTGACG      250
TGTCCGGCAA CATCCTCAAC AAGAAGGCCG ACGAGACCGT TAAGGTTACC      300
GAACGTTGGT CTATCCACCG TAACCCGCCG GCATTGACC AGCTGGAGTC      350
CAAGACCCAG ATGTTTCGAAA CCGGTATCAA GGTCATCGAT TTGCTGACCC      400
10 CGTATGTGCA GGGCGGCAAG ATCGGTCTGT TCGGCGGCGC AGGCGTCGGC      450
AAGACCGTGC TGATCCAGGA AATGATTGAG CGTGTGGCTC AGAACCACGG      500
CGGTGTGTCC GTGTTTCGAG GCGTCGGCGA GCGTACCCGT GAGGGTAACG      550
ATCTGATCGG CGAAATGGAC GAAGCCGGCG TGCTCGAGAA GACCGCACTG      600
GTCTTCGGCC AGATGGATGA GCAGCCGGGT ACCCGTCTGC GCGTGCCGCT      650
15 GACCGCACTG ACCATGGCAG AGTACTTCCG TGACGTACAG AATCAGGACG      700
TGCTGCTGTT CATCGATAAC ATCTTCCGTT TCACCCAGGC TGGTTCCGAG      750
GTGTCCACCC TGCTCGGCCG TATGCCGTCC GCAGTGGGCT ACCAGCCGAA      800
CCTGGCCGAT GAGATGGGCG CGCTGCAGGA GCGAATCACT TCGACCCGTC      850
GACACTCCAT CACCTC      866
20

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2) INFORMATION FOR SEQ ID NO: 255

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 842 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Brucella abortus
35 (B) STRAIN: S2308

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

```

AAGGCCAGCT GCCGCTGATC CTGAACGCGC TTGAAGTGGA CAATCAGGGC      50
40 CATCGTCTGG TTCTCGAAGT TGCCCAGCAC CTCGGCGAAG ACACCGTGCG      100
CACCATCGCC ATGGACGCGA CCGAAGGTCT CGTTCGCGGT CAGGAAGCAC      150
GCGACACTGG CGAACCGATC ATGGTGCCGG TCGGCGTCGA AACGCTTGGC      200
CGCATCATGA ACGTCATCGG CGAGCCGGTT GACGAAGCAG GCCCCATCAA      250
GACCAAGGCA ACCCGCGCCA TCCACCAGAA CGCGCCGGAA TATATCGAAC      300
45 AGTCGACCGA AGCCGAAATT CTGGTCACGG GCATCAAGGT CGTCGACCTT      350
CTGGCGCCTT ACGCCAAGGG CGGCAAGATC GGCTCTTCG GCGGTGCAGG      400
CGTCGGCAAG ACCGTTCTCA TCATGGAAC CATCAACAAC GTCGCCAAGG      450
CGCACGGCGG TTATTCCGTG TTCGCAGGCG TCGGTGAGCG TACCCGTGAG      500
GGCAACGACC TTTACCACGA AATGATCGAG TCGGGCGTGA ACAAGCTCGG      550
50 CGGCGGCGAA GGCTCCAAGG CAGCCCTCGT TTACGGCCAG ATGAACGAAC      600
CCCCGGGTGC CCGCGCCCGC GTTGCCCTTT CCGTCTGAC GGTGCTGAA      650
AACTTCCGTG ACCAGGGCCA GGACGTTCTG TTCTTCGTGG ACAACATCTT      700
CCGCTTCACG CAGGCAGGTT CGGAAGTGTC GGCTCTTCTC GGCCGTATTG      750
CTTCCGCTGT GGGTTATCAG CCGACGCTGG CAACCGACAT GGGCGCCATG      800
55 CAGGAACGCA TCACCACGAC GACCAAGGGT TCGATCACCT CG      842

```

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```

15  CGAGTTCCTT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTTCT TCCGACGGTC TCGTTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
20  GGCGATATCG GCGAAGAAGA CCGTTGGGCT ATTCACCGCG CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGCGG GCGTGGGTAA AACCCTAAAC ATGATGGAGC TTATCCGTAA      450
    CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC      500
25  GTACTCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCGTG      650
    ACGAAGGTCG TGACGTTCTG CTGTTCTGTTG ATAACATCTA CCGTTACACC      700
    CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCTGATGC CTTCTGCGGT      750
30  AGGTTACCAG CCAACTCTGG CGGAAGAGAT GGGTGTCTTT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                               833
  
```

2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG      150
    GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
55  TCTGGGTCTG ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAAGTCTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT      400
    GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
50  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
  
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TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGACTCC	AACGTTCTGG	550
ACAAAGTTGC	ACTGGTTTAC	GGCCAGATGA	ACGAGCCGCC	AGGTAACCGT	600
CTGCGCGTAG	CGCTGACCGG	TCTGACCATC	GCGGAGAAAT	TCCGTGACGA	650
AGGCCGTGAC	GTTCTGCTGT	TCGTGATAA	CATCTATCGT	TATACCCTGG	700
CCGGTACAGA	AGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGT	750
TATCAGCCTA	CTCTGGCAGA	AGAGATGGGT	GTTCTTCAGG	AGCGTATTAC	800
CTCCACCAAG	ACCGGTTCCA	TCACTTCCG			829

10

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
(B) STRAIN: ATCC 33855

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

TCCCTCAGGA	CGGCGTACCG	CGCGTTTATG	ACGCGCTTGA	GGTACAGAAC	50
AACAATGAGA	AGCTGGTGCT	GGAAGTTCAG	CAGCAGCTCG	GCGGCGGTAT	100
CGTGCGTACC	ATCGCAATGG	GTTCTTCCGA	CGGTCTGCGT	CGTGGTCTGG	150
30 TAGTAACAGA	CCTCGAGCAC	CCGATCGAAG	TCCCGGTAGG	TAAAGCGACC	200
CTTGGCCGTA	TCATGAACGT	GCTGGGTCAG	CCGATCGACA	TGAAAGGCCGA	250
CATCGGCGAA	GAAGACCGTT	GGGCGATTCA	CCGCGCAGCA	CCTTCCTAEG	300
AAGAGCTGTC	CAGCTCTCAG	GAATTGCTGG	AAACCGGCAT	CAAAGTTATC	350
GACCTGATTT	GTCCGTTTCG	TAAGGGCGGT	AAAGTAGGTC	TGTTCCGGTGG	400
35 TGCGGGCGTA	GGTAAAACCG	TAAACATGAT	GGAGCTGATC	CGTAACATTG	450
CGATCGAGCA	CTCCGTTTAT	TCCGTGTTTG	CGGGCGTGGG	TGAGCGTACT	500
CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACCGACTCCA	ACGTTCTGGA	550
TAAAGTAGCA	CTGGTTTACG	GCCAGATGAA	CGAGCCACCA	GGTAACCGTC	600
TGCGCGTAGC	GCTGACCGGT	CTGACCATCG	CGGAAAAATT	CCGTGACGAA	650
40 GGCCGCGACG	TTTTGCTGTT	CGTTGATAAC	ATCTACCGTT	ATACCCTGGC	700
CGGTACCGAA	GTATCTGCAC	TGCTGGGTCG	TATGCCTTCT	GCGGTAGGTT	750
ATCAGCCAAC	TCTGGCAGAA	GAGATGGGTG	TTCTTCAGGA	GCGTATTACC	800
TCCACCAAGA	CCGGTTCTAT	CACCTCCGTA			830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 931 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
(B) STRAIN: CDC B7681

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAACATT	TATGACGCAC	TTGAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCGCAG	GAGTAGGTGA	500
	GAGAACAAGA	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTCT	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGAG	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACTTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACTCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

25 2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAGTG	GGTCTGTTCG	300
	GTGGTGC GGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TACTCCGTG	TTTGC GGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTC	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCTG	GACGTACTGC	TGTTCTGTCG	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCTGATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCTGGC	GGAAGAGATG	GGTGTTCCTG	AGGAACGTAT	700
55	CACTTCTACC	AAAACCGGTT	CTATCA			726

2) INFORMATION FOR SEQ ID NO: 261

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
    CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
20  AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
    TCCGTTTACT CCGTGTTTGC GGGCGTGGGT GAACGTAATC GTGAGGGTAA      500
25  CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
    TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC      750
30  CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAC      800
    CGGTTCTATC AC                                     812
  
```

2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTAC GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCTTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
55  TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTCC      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAAACC      400
    GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
50  CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT      500
  
```

	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	CCTGGTTTAC	550
	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	CGCTGACCGG	600
	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGTCGTGAC	GTTCTGCTGT	650
	TCGTCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACGGA	AGTATCCGCA	700
5	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TACCAGCCGA	CCCTGGCGGA	750
	AGAGATGGGT	GTTTTGCAGG	AACGTATCAC	CTCCACCAAA	ACCGGTTCTA	800
	TCACCTCCGT	A				811

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
(B) STRAIN: ATCC 51112

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTTATGA	ATGGTAAAGA	50
	GAGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGT	ATCGTACGTA	100
	CCATCGCGAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GGAAGTAAAA	150
30	GACCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CTCTGGGTCG	200
	TATCATGAAC	GTCCTGGGTC	ACCCGATCGA	CATGAAAGGC	GATATCGGTG	250
	AAGAAGAGCG	TTGGGCTATC	CACCGCGCAG	CGCCATCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGT	GGTGCGGGTG	400
35	TAGGTAA AAC	CGTAAACATG	ATGGA ACTCA	TCCGTAA CAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCCGTGTT	TGCGGGCGTA	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTTCTG	GATAAAGTAT	550
	CCCTGGTATA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCAGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
40	CGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCAT	CAGCGGTAGG	CTACCAGCCA	750
	ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CTTCTACCAA	800
	AACCGTTTCT	ATTACC				816

45

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
(B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```

AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG      100
5  TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA      150
AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT      200
CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG      250
TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC      300
TGTCAAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG      350
10 ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCG GTGGTGCGGG      400
TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG      450
AACACTCCGG TTA CTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG      500
GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTC TGGACAAAGT      550
ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG      600
15 TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT      650
GACGTTCTGC TGTTCTGTTGA TAACATCTAT CGTTACACCC TGGCCGGTAC      700
AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC      750
CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC      800
AAAACCGGTT CTATCACCT      819
20

```

2) INFORMATION FOR SEQ ID NO: 265

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 822 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Citrobacter koseri
35 (B) STRAIN: ATCC 27028

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```

GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
40 ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATCGTACGTA      100
CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA      150
GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCTG      200
TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG      250
AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG      300
45 TCAAACCTCT AGGAACTGTT GGAAACCGGT ATCAAAGTTA TCGACCTGAT      350
GTGTCCGTTT GCGAAGGGCG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG      400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA      450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG      500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
50 CCTTGGTTTA CGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT      600
GCGCTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGTCGTGA      650
CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCTGT GCGGTCACCG      700
AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG      750
ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA      800
55 AACCGGTTCT ATCACCTCCG TA      822

```

2) INFORMATION FOR SEQ ID NO: 266

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15 GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA      50
   GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA      100
   CCATCGCCAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCG      200
   TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG      250
20 AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG      300
   TCTAACTCTC AGGAAGTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT CGGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGCG      400
   TAGGTAA AAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
25 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
   CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC      600
   GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG      700
   AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750
30 ACTCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCAACCAA      800
   AACCGGTTCT ATCACCTCCG                                     820

```

35 2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

50 GCCGTACCGC GCGTGACGTA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
   CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
   TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC      150
   CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCGTAT      200
55 CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
   AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC      300
   AGTTCTCAGG AACTGCTGGA AACCAGGCATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTCCGC AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
50 TCCGGTTACT CAGTGTTTGC GGGCGTTGGT GAACGTACTC GTGAGGGTAA      500

```

CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
CTGACCGGTC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5 TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAAC	800
CGGTTC					806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
(B) STRAIN: ATCC 29935

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30 CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
AAGAGCGTTG	GGCTATTAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
35 GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
10 ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAAC	800
CGGTTCTATC					810

15

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5   TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
    AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA      100
    ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
    TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
    ATTCTGGGAA GAATGTTCAA TGTCCTCGGA CGTGAAATTG ATGGTCTGGG      250
    ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
    TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10  ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
    TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
    TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
    ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
    TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15  GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
    CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
    CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
    TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
    ATTACATCCA CGAAGGATGG TTCCATT      827
20

```

2) INFORMATION FOR SEQ ID NO: 270

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40  GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
    CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
    TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
    GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
    ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
    AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATT      300
15  GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
    CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
    GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
    GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
    AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
50  AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
    ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
    AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTGAGA TTCTACAAG      700
    CTGGATCAGA GTTTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
    TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
55  ATCAACTACC CATGGATCAA TTACATCAG      829

```

2) INFORMATION FOR SEQ ID NO: 271

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

TTGTCCACGT TGGATRTCTT CA

22

2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30	CCCGCGTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
	CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
	GGCGACAACC	TCGTTGCGGC	CGTGTCCATG	GCCCCTACCG	ACGGCCTCGT	150
	CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35	CGGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
	GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
	ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
	TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
	CTGTTTCGGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40	CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
	GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
	GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
	AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
	TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45	CGTTTACCCC	AGGCCGGTTC	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
	TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTCTTCC	800
	AGGAGCGTAT	TACCTCTA				818

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

	CGATGCCTGC	TCTGTACAAC	GCGCTGACTG	TCGAGGTCAC	CCTCGAGGCA	50
	GTCGCCAAGA	CCATCACGCT	TGAGGTTGCA	CAGCACCTCG	GCGATAACCT	100
	GATCCGGACC	ATTGCGTTGG	CACCTACGGA	CGGTCTCGTC	CGTGGCGCTG	150
10	AGGTTATCGA	CACTGGTAAG	CCAATTACTG	TTCCCGTCGG	CGATGCCGTC	200
	AAAGGACACG	TCTTCAATGC	GCTCGGTGAG	TGTTTGGACG	AACCAGGATT	250
	GGGCCGCGAC	GGCGAACAGT	GGGGAATCCA	CCGCGATCCG	CCACCATTTCG	300
	ATGCGCTGGA	GGGCAAAACC	GAGATTCTGG	AGACTGGAAT	CAAGGTTATC	350
	GACCTCCTTA	CCCCTTACGT	TAAGGGTGGC	AAAATTGGTC	TGTTTCGGTGG	400
15	CGCCGGCGTC	GGCAAGACCG	TTCTTATCCA	GGAAATGATC	ACTCGTATCG	450
	CTCGTAACTT	CTCCGGTACT	TCCGTGTTTCG	CCGGCGTCGG	TGAGCGTACC	500
	CGTGAGGGTA	CTGACCTGTT	CCTGGAAATG	GAAGAGATGG	GCGTGTTCGA	550
	AGACACCGCC	CTTGTCTTCG	GTCAAATGGA	CGAACCACCA	GGGGTTCGTA	600
	TGCGCGTGGC	CTTGTCTGGT	CTAACCATGG	CTGAATATTT	CCGCGACGTT	650
20	CAAAACCAGG	ACGTTTTGTT	GTTTATTGAC	AACATCTTCC	GTTTTACTCA	700
	GGCAGGTTCC	GAGGTTTCCA	CGCTGTTGGG	CCGTATGCCT	TCCGCCGTGG	750
	GTTATCAGCC	AACATTGGCT	GATGAGATGG	GTGTTTTGCA	GGAACGGATT	800
	ACCTCTACAC	GTGGTAAGTC	AATTACTTCC	CTG		833

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

	CCGTGCTCAT	CCAGGAGATG	ATCACCCGTG	TGGCCCGCAA	CTTCGGCGGC	50
	ACCTCTGTGT	TCGCCGGCGT	CGGCGAGCGC	ACCCGTGAGG	GCAACGACCT	100
15	CTGGGTCGAG	ATGGACGAGG	CCGACGTGCT	CAAGGACACC	GCCCTGGTGT	150
	TCGGCCAGAT	GGACGAGCCG	CCGGGAACCC	GTCTGCGCGT	GGCCCTGTCC	200
	GCGCTGACCA	TGGCGGAGTA	CTTCCGCGAT	GTGCAGAACC	AGGACGTGCT	250
	GCTGTTTCATC	GACAACATCT	TCCGCTTCTC	CCAGGCCGGC	TCCGAGGTCT	300
	CCACCCTGCT	GGGCCGCATG	CCCTCCGCGG	TGGGCTACCA	GCCGAACCTG	350
50	GCGGACGAGA	TGGGTGTGCT	GCAGGAGCGC	ATCACCTCGA	CTCGCGGCCA	400
	CTCCATCACC	TCGATGC				417

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10
 GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50
 GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100
 ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150
 GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200
 15 TGTCAAGGGG CACGTCTTCA ACGCCCTGGG CACTGCTGCTG GATGAGCCAG 250
 GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300
 TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350
 CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400
 GTGGTGACAG TGTGGGTAAAG ACCGTCTCTGA TTCAGGAGAT GATTACCCGT 450
 20 ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500
 TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC 550
 TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600
 CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650
 TGTTCAAGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700
 25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750
 GTGGGTTACC AGCCGACCCT GGCTGACGAG ATGGGTGTTT TGCAGGAGCG 800
 CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

30
 2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50
 AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100
 AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150
 50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTAGGTCGT 200
 ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250
 AAAAGAAAAA CTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300
 CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350
 TGCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400
 55 TGGAAAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450
 ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500
 AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550
 GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600
 GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650
 50 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTGTA 700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

	TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
	CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25	TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
	GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCTGTGTTG	GCAAGGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
	AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
	GAAGATCTGT	CTAACTCTCA	GGAAGTGTG	GAGACCGGCA	TTAAGGTTAT	350
30	CGACCTGATT	TGCCCCGTTG	CTAAAGGCGG	TAAAGTGGGC	CTGTTGCGGTG	400
	GGGCCGGTGT	GGGTAAGACC	GTTAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
	CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
	ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35	CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
	AGGTCGTGAT	GTACTGTTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
	CCGGTACTGA	AGTCTCCGCT	CTGTGGGGCC	GTATGCCGTC	GGCGGTAGGT	750
	TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
40	CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

	GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50	ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTCGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCCGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTGACAT	GAAGGGCGAG	ATCGGCCAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTGCGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTT	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
- (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTCAATCAAT	TTGCACCTAA	GTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCGGT	ATTCGCCGGT	GTGGGTGAGC	GTAATCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10
 GCCGTACCAC GAGTGTACGA TGCACTTGAG GTAAAGAATG GTGAAGAGCG 50
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CCGTGCGGTT GTACGTACCA 100
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCGATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 20 TCCGTTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
 TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAAGTTC CGTGACGAAG GTCGTGACGT 650
 ACTGTTGTTC GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CGG 803

30
 2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
 GGTATCGTAC GTACTATCGC CATGGGTCTT TCCGACGGTC TCGCTCGTGG 150
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCC G TAGGTAAG 200
 CAACACTGGG TCGTATCATG AACGTTTGG GTCAACCAAT CGACATGAA 250
 GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
 CTATGAAGAG CTGTCTAGCT CTCAGGAAC GCTGGAAACC GGCATCAAAG 350
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
 55 GCGGGTGC GGCTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
 CCGTCTGCGC GTTGCCTGA CCGGTCTGAG TATGGCTGAG AAGTTCCGTG 650
 50 ACGAAGGTCG TGACGTACTG CTGTTCTGTAG ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25 TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30 TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTTG	400
GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35 CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
CGGTTCTATC					810

40

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60 CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAAC	800
15	CGGTTCTATC	A				811

2) INFORMATION FOR SEQ ID NO: 284

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
40	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
45	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTT	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTCTATC	ACTTCCG				817

2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50
 GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100
 TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150
 GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200
 15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250
 AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC 300
 CTGATTGCGC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350
 GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400
 TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGCGGTGA ACGTACTCGT 450
 20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500
 AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGA AACCGTCTGC 550
 GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600
 CGTGACGTTT TGCTGTTTCG CGATAACATC TACCGCTATA CCCTCGCCGG 650
 TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTACC 700
 25 AGCCGACGCT GGC GGAAGAG ATGGGTGTTT TGCAGGAACG TATCACCTCC 750
 ACCAAAACCG GTTCTA 766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45 GCCGTACCAC GCGTGACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150
 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
 50 CATGAACGTA TTGGGTACAG CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTACGA AGAGCTGTCC 300
 AGCTCTCAGG AACTGCTGGA AACC GG CATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 55 TCCGTTTACT CCGTGTTTGC GGGCGTGGGT GAACGTA CTG GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
 TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
 TCTGCTGTTT GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 50 TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTAA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasakii*
(B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

	TACGACGCCC	TTGAGGTAAC	GAATGGTAAT	GAGCGTCTGG	TGCTGGAAGT	50
	CCAGCAGCAG	CTCGGCGGCG	GTATCGTACG	TACCATCGCG	ATGGGCTCTT	100
	CCGACGGTCT	GCGTCGCGGT	CTGCCTGTTG	CAGACCTTGA	GCACCCGATC	150
25	GAAGTGCCGG	TAGGTAAAGC	GACGCTGGGT	CGTATCATGA	ACGTCCTGGG	200
	TCAGCCTATC	GACATGAAAG	GCGACATCGG	CGAAGAAGAG	CGTTGGGCGA	250
	TTCATCGCGC	GGCGCCGTCC	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	300
	CTGGAACCG	GCATCAAAGT	TATCGACCTG	ATGTGTCCGT	TCGCGAAGGG	350
	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCAGG	TGTAGGTAAA	ACCGTAAACA	400
30	TGATGGAGCT	TATTCGTAAC	ATCGCGATTG	AGCACTCCGG	TTACTCCGTG	450
	TTTGCGGGCG	TGGGCGAACG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	AATGACCGAC	TCCAACGTAC	TGGATAAAGT	ATCCCTGGTG	TACGGCCAGA	550
	TGAACGAGCC	GCCGGGAAAC	CGTCTGCGCG	TTGCGCTGAC	CGGCCTGACC	600
	ATGGCTGAGA	AATTCCGTGA	CGAAGGTCGT	GACGTTCTGC	TGTTCTGTCGA	650
35	CAACATCTAC	CGTTACACCC	TGGCCGGTAC	TGAAGTATCC	GCACTGCTGG	700
	GCCGTATGCC	TTCAGCGGTA	GGTATCAGC	CGACCCTGGC	GGAAGAGATG	750
	GGTGTTCCTGC	AGGAGCGTAT	CACCTCCACC	AAAACCGGTT	C	791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

	TTTCTTTAGA	TCAATCCTTA	CCAGACATCA	ACAATGCGTT	GATTGTTTAC	50
	AAAAAAGATA	AAACAAAAGT	TGTTCTTGAA	GTTGCTTTGG	AACTTGGTGA	100
	TGGTGTTATC	CGCACAAATCG	CTATGGAGGC	TACTGATGGA	TTGCAACGTG	150
50	GAATGGAAGT	TGTCGATACT	GGCAAATCAA	TCTCCGTTCC	TGTAGGTAAA	200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGGG	AACAGGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCGGTGTT	GCCGGTGTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTCGG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTGACC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 847 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTGTTGA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGACAA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTACTTCCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
50	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

2) INFORMATION FOR SEQ ID NO: 290

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*

(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

	TTTCTTTAGA	CCAATCCTTA	CCAGATATCA	ACAACGCTTT	AGTTGTTTAT	50
10	AAAAATGATG	AGAAGAAATC	GAAAGTTGTT	CTTGAAACAG	CGCTAGAATT	100
	AGGTGACGGT	GTCATCCGTA	CAATCGCGAT	GGAATCAACA	GATGGTTTAC	150
	AACGCGGAAT	GGAAGTCATT	GATACAGAAA	AAGCAATTTT	TGTACCAGTG	200
	GGTAAAGAAA	CGTTAGGTCG	TGTATTCAAT	GTATTAGGAG	ATACGATCGA	250
	TTTATCTGCA	CCTTTCCCAG	AAGATGCAAA	ACGTAGCGAA	ATCCATAAAA	300
15	AAGCACCAAA	CTTTGATGAG	TTAAGTACAA	GTACTGAGAT	CCTTGAAACT	350
	GGGATCAAAG	TTATTGACTT	GCTTGCTCCT	TACTTAAAG	GTGGGAAAGT	400
	TGGATTATTC	GGTGGTGCCG	GTGTAGGTAA	AACTGTATTG	ATCCAAGAAT	450
	TGATCCATAA	TATCGCTCAA	GAACACGGTG	GTATTTCTGT	ATTTACTGGT	500
	GTTGGTGAAC	GTACACGTGA	AGGTAATGAC	CTTTATTATG	AAATGAAAGA	550
20	TTCAGGAGTT	ATTGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	600
	CACCAAGTGC	ACGTATGCGT	GTTGCCTTGA	CTGGTTTGAC	GATTGCTGAA	650
	TACTTCCGTG	ATGTTGAAGG	GCAAGACGTG	CTATTGTTTA	TTGATAATAT	700
	TTTCCGTTTC	ACTCAAGCCG	GTTCAGAAGT	TTCTGCCCTA	TTAGGTCGTA	750
	TGCCTTCTGC	CGTTGGGTAC	CAACCAACGC	TAGCAACAGA	AATGGGTCAA	800
25	TTACAAGAAC	GGATCACTTC	AACGAAAAAA	GGTTCAATCA	CTTCA	845

2) INFORMATION FOR SEQ ID NO: 291

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

15	TTAGATCAAT	CCTTACCCGA	TATTAACAAC	GCTTTAGTCG	TTTATAAAAA	50
	TGGCGAAGCA	AAACAAAAAG	TAGTACTTGA	AGTCGCTTTA	GAAGTAGGTG	100
	ATGGAGTGAT	TCGTTCTATC	GCCATGGAAT	CGACAGATGG	TTTACAACGT	150
	GGAATGGAAG	TTATCGATAC	AGGAAAATCA	ATTTCAAGTT	CTGTTGGTAA	200
	AGATACATTA	GGTCGTGTGT	TTAACGTTTT	AGGAGACACA	ATTGACTTAG	250
50	AAGCGCCATT	CCCTGCAGAT	GCTGAACGTA	GTGGGATTCA	TAAAAAAGCG	300
	CCAGCATTTG	ATGAATTAAG	TACCAGTAAT	GAAATTTTAG	AAACAGGGAT	350
	TAAAGTTATT	GACTTATTAG	CACCTTATCT	AAAAGGTGGT	AAAGTCGGAC	400
	TTTTTCGGTGG	TGCCGGTGTT	GGTAAAACCG	TCTTAATTCA	AGAATTAATT	450
	CATAATATTG	CCCAAGAACA	TGGAGGGATT	TCCGTCTTTA	CTGGTGTTGG	500
55	TGAACGGACA	CGTGAAGGGA	ACGATCTGTA	CTATGAAATG	AAAGATTCAG	550
	GCGTTATTGA	AAAAACAGCC	ATGGTTTTTG	GTCAAATGAA	CGAACCGCCA	600
	GGTGCACGGA	TGCGTGTGGC	CTTAACCTGG	TTAACGATTG	CTGAATATTT	650
	CCGTGATGTG	GAAGGACAAG	ACGTGCTATT	ATTTATTGAT	AACATTTTCC	700
	GTTTCACCCA	AGCCGGTTCA	GAAGTTTCTG	CCCTTTTAGG	TCGGATGCCG	750
50	TCAGCCGTTG	GTTACCAACC	AACCTTAGCG	ACTGAAATGG	GACAATTACA	800

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCTGTGA 200
 25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
 TTTAGAAACA CCTTTCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
 GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
 30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
 TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
 35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
 TGCCTTCTGC GGTGGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
 TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
 60 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTCCGGTGG	400
5	TGCCGGTGT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTGTTG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGACTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGGTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTT	TGTTCTCTGT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCACT	ATTTGCGGGT	500
	GTTGGTGAGC	GTACTCGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTTGACAA	ATGAACGAAC	600
45	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTTCAAGAT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

2) INFORMATION FOR SEQ ID NO: 295

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*

(B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

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10  GCCGTACCGC GCGTGACGA TGCTCTTGAG GTGCAAAATG GTAATGAGCG      50
    TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGTGGTATC GTGCGTACCA      100
    TCGCAATGGG GTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAC      150
    CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT      200
    CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG      250
    AAGAGCGTTG GGCGATTAC CCGCAGCAC CTTCTACGA AGAGCTGTCA      300
15  AACTCTCAGG AACTGCTGGA AACC GG TATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAACTGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
    TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CTGACTCCAA CGTTATCGAC AAAGTATCCC      550
20  TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA      600
    CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTT GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
    TATCCGCACT GCTGGGCCGT ATGCCTTCAG CGGTAGGTTA TCAGCCGACT      750
    CTGGCGGAAG AGATGGGCGT TCTTCAGGAA CGTATCACCT CCACCAAAC      800
25  TGG                                     803

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2) INFORMATION FOR SEQ ID NO: 296

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*

(B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

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45  GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA ATGGTGATGA      50
    GCGTCTGGTG CTGGAAGTGC AGCAGCAGCT CGGCGGCGGT ATCGTGCGTA      100
    CCATCGCAAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GACTGTCGTC      150
    GACCTCGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCGA CCCTGGGCCG      200
    TATCATGAAC GTGCTGGGTC AGCCGATCGA CATGAAAGGC GATATCGGTG      250
50  AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCGTCCTA TGAAGAGCTG      300
    TCCAGCTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
    GTGTCCGTTT CGGAAGGCGG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGCG      400
    TAGGTAAAAC GCTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
    CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
55  TAACGACTTC TACCATGAAA TGACCGACTC CAACGTTCTG GACAAAGTAT      550
    CCCTGGTTTA CGGCCAGATG AACGAACCGC CGGGAAACCG TCTGCGCGTT      600
    GCACTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTTCTGTTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACTG      700
    AAGTATCCGC ACTGCTGGGC CGTATGCCTT CTGCGGTAGG TTACCAGCCG      750
50  ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAGCGTATCA CCTCCACCAA      800

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AACCGGTTCT ATCACCTCCG TA

5 2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
 GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
 TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
 CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
 25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
 GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
 CAGGAACTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
 CGCCAAGGGC GGTAAAGTCG GCCTGTTCCG CGGCGCGGGC GTGGGTAAAA 400
 CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450
 30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
 CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
 ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCCTGACC 600
 GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
 GTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700
 35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
 GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTT 800
 TATCACCT 808

40

2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 (B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTAC AACGCGCTGA CGGTTGATGC 50
 CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
 TGCCGGGCAA CCTTGTCGCG TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
 50 GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200

	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGTCG	250
	ACGAGAAGCC	GATGCCCAG	GTGAAGGGCT	ACATGCCCAT	CCACCGTCCG	300
	GCTCCGGACT	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTCCG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTCGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTTCG	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

50

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*

(B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

	AACACGCCTA	AAGTATATGA	TGCTTTAAAT	GTAGTAGAAG	CTGGTTTAGT	50
10	ATTAGAAGTT	CAGCAACAAA	TTGGTGATGG	CGTAGTTCGT	ACAATTGCTA	100
	TGGGATCTAG	TGATGGTCTT	AGACGTGGTA	TGGAAGTTAA	GAACACAAAT	150
	GCGCCTATTT	CTGTTCCAGT	TGGACATGGC	ACACTTGGAC	GTATCATGAA	200
	TGTTTTAGGT	GAACCAATTG	ATGAAGCTGG	TCCAATTGAA	TATACTGAGA	250
	AAAGATCTAT	CCATCAAGCT	CCTCCTGCAT	ATGATGAGTT	AGCATTAAAGT	300
15	ACAGAAATAT	TAGAAACAGG	TATCAAAGTA	GTTGACCTTA	TTTGTCCATT	350
	TGCTAAGGGC	GGTAAAGTTG	GTTTATTTGG	CGGTGCAGGT	GTTGGTAAAA	400
	CTGTAACGAT	GATGGAACCT	ATCAACAATA	TTGCAAAAGA	ACATAGTGGC	450
	TACTCTGTAT	TTTCCGGTGT	TGGTGAAAGA	ACTCGTGAAG	GTAATGACTT	500
	CTACTATGAG	ATGAAATATT	CTAATGTATT	GGATAAAGTA	TCATTAGTAT	550
20	ATGGTCAGAT	GAATGAGCCG	CCTGGAAACA	GATTAAAGAGT	AGCTCTTAGT	600
	GGCTTAACAA	TAGCAGAAGG	ATTCCGTGAT	GAAAAGCGTG	ATGTTTTGAT	650
	GTTTATCGAT	AACATCTATC	GTTATACATT	AGCAGGTACA	GAGGTATCGG	700
	CGCTACTTGG	TCGTATGCCA	TCTGCTGTGG	GTTATCAGCC	AACGCTTGCA	750
	GCTGAGATGG	GTGCTTTACA	GGAGCGTATT	ACATCTACTA	AGACAGGATC	800
25	TATTA					805

2) INFORMATION FOR SEQ ID NO: 301

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusobacterium gonidiaformans*

(B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

45	GACGAATTGC	CAAAAATATA	CAATGCATTA	AAGGTGCAAG	TTGGAGAAAA	50
	AGAACTTGTA	TTGGAAGTGC	AACAACATTT	GGGAAATAAT	GTTGTGAGAA	100
	CAGTAGCGAT	GGACTCAACA	GATGGATTGC	TTCGAGGAAT	GGAAGTAATG	150
	GATACCGGAG	CACCGATTAC	TGTTCAGTA	GGGAAGGCGG	TTTTAGGAAG	200
	AATATTGAAT	GTTTTGGGAG	AGCCTGTGGA	TCAAAAAGGG	CCTGTGGAAA	250
50	CAGAAGAATA	TTTACCTATC	CATAGAGAAG	CACCAAAATT	TGAAGAACAA	300
	GAAACAGTAA	CAGAAATTTT	TGAAACAGGA	ATTAAAGTCA	TAGATTTGTT	350
	AGCCCCTTAT	ATCAAAGGAG	GAAAGACAGG	TCTATTCGGT	GGAGCCGGAG	400
	TAGGGAAAAC	AGTTTTAATT	ATGGAATTAA	TTAATAACAT	TGCAAAGGGC	450
	CACGGAGGAA	TTTCTGTGTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
55	AAGAGATTTA	TACAACGAAA	TGACAGAGTC	CGGAGTTTTG	AATAAGACCT	550
	CGTTGGTGTA	TGGTCAAATG	AATGAGCCGC	CCGGAGCAAG	ACTTCGTGTG	600
	GCGTTGACAG	GATTAACGGT	TGCTGAAAAC	TTTAGAGATA	AAGAAGGGCA	650
	AGATGTATTG	TTGTTTATCG	ACAATATCTT	CCGTTTCACA	CAAGCAGGAT	700
	CAGAAGTATC	GGCTCTATTG	GGAAGAATTC	CATCGGCAGT	AGGATATCAA	750
60	CCGAACCTAG	CGACAGAAAT	GGGAACCTTA	CAAGAAAGAA	TTACTTCTAC	800

AAAATCAGGA TCTATCACTT CGGTA

5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp.
necrophorum
 (B) STRAIN: ATCC 25286

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

	ACAATGCATT	AAAGGTACAG	GTGGGAGAAA	GGGAAGTGT	GTTGGAAGTG	50
	CAGCAACATT	TAGGAAATAA	TGTTGTCAGA	ACAGTAGCAA	TGGATTCAAC	100
	AGACGGATTA	CTTCGGGGAA	TGGAAGTGAG	AGATACAGGA	GTTCCCATTA	150
25	CTGTTCCGGT	AGGAAAGGCG	GTTTTGGGAA	GAATATTTAA	TGTCTTAGGG	200
	GAGCCTGTGG	ACGAAAAAGG	TCCGATAGAG	ACAGAAGAAT	ATTTACCAAT	250
	ACATAGAGAA	GCACCGAAAT	TTGAAGAACA	GGAAACGGTG	ACAGAAATTT	300
	TTGAAACAGG	AATTAAAGTC	ATTGATTTGT	TAGCTCCTTA	TATTAAAGGA	350
	GGAAAAACAG	GCCTATTCGG	AGGAGCCGGA	GTAGGAAAAA	CCGTTTTGAT	400
30	TATGGAAGTG	ATCAATAATA	TTGCAAAAGG	TCATGGAGGA	ATTTCTGTTT	450
	TTGCAGGAGT	TGGAGAAAGA	ACGAGAGAGG	GAAGAGATCT	ATACAACGAA	500
	ATGACAGAGT	CCGGAGTTTT	GAATAAAACT	TCTTTGGTAT	ATGGGCAAAAT	550
	GAATGAGCCG	CCCGGAGCAA	GACTTCGAGT	GGCTTTAACC	GGACTTACTG	600
	TTGCCGAAAA	TTTCAGAGAT	AAAGAGGGAC	AGGATGTCTT	ATTGTTTATT	650
35	GACAAATATTT	TCCGTTTCAC	ACAAGCAGGT	TCGGAAGTAT	CGGCACTTTT	700
	GGGGAGAATT	CCTTCTGCAG	TGGGATATCA	ACCGAACTTG	GCGACAGAAA	750
	TGGGAAGCTT	ACAAGAAAGA	ATTACTTCTA	CAAAATCCGG	TTCTATCACT	800
	TCCGTG					806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

	GATGAATTGC	CTGCAATATA	TAATGCTTTA	AAAGTAAAAT	TAGAAGATAA	50
	GGAAGTTGTT	CTAGAAGTTG	AACAACATCT	TGGTAACAAT	GTTGTAAGAA	100
50	CTGTTGCTAT	GGATTCAACT	GATGGATTAA	AAAGAGGAAT	GGAAGTTATA	150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTTTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACCTA	TCAACAACAT	TGCAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCATTAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821

2) INFORMATION FOR SEQ ID NO: 304

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 864 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Gardnerella vaginalis*
 - (B) STRAIN: ATCC 49145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACCGCAA	CCCACCTGCT	TTCGATCAGC	TTGAGTCTAA	350
	GACTCAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTG	CTTACGCCTT	400
	ACGTTTCAGGG	CGGAAAGATT	GGTCTGTTCG	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTCAGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACG	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTGAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCTCTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTGAGAA	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

55 2) INFORMATION FOR SEQ ID NO: 305

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 848 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10 TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA 50
 GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT 150
 TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT 200
 15 GTAGGTAAGT ACACATTAGG TCGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA 300
 AAGAAGCTCC AACATTTCGAT GAATTATCAA CTCACGTTGA GGTTCCTTGAA 350
 ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA 400
 AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG 450
 20 AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA 500
 GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA 550
 AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG 600
 AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAAATGGCG 650
 GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA 700
 25 CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTCCTGCG TTATTAGGAC 750
 GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA 800
 CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT 848

30 2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA 50
 GAAAAAGGCG ATGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT 150
 50 TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA 200
 GTAGGTAAGT ATACATTAGG ACGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTGATA 300
 AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA 350
 ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA 400
 55 GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG 450
 AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT 500
 GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTACT ATGAAATGAA 550
 AGACTCTGGA GTTATTAATA AACTGCCAT GGTATTTGGT CAAATGAATG 600
 AGCCACCAGG TGCACGTATG CGTGTTGCCT TAACAGGATT AACAAATGGCA 650
 50 GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA 700

TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

5

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAAAC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
AATCACGGCA	GTA				813

10

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 55 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCTTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTGCGAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGCG	400
	GGGTAGAGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCGTG	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

2) INFORMATION FOR SEQ ID NO: 309

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCAT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTTGG	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAACA	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCT	AGCAGGTACG	GAAGTGTCAG	700
	CACTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

```

10 CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG      50
   AATCGGGTTT AACCCCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA      100
   CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT      150
   TGAAAATACC AATAAACCAA TTTCAGTACC GGTGTTGGTGTG AAAACTCTCG      200
15  GTCGTATTAT GAACGTATTG GCGCAACCGA TTGATGAAAG AGGTCCCTATC      250
   GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA      300
   ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT      350
   TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG      400
   GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT      450
20  TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG      500
   AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA      550
   GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG      600
   TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC      650
   GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG      700
25  ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA      750
   GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA      800
   CCAAACAGG TTCTATTACT TCTG                                     824

```

30 2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

```

   GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA      50
   ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA      100
   TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC      150
50  CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT      200
   TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCCAAG      250
   AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT      300
   AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG      350
   TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTTG      400
55  GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
   TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTA CTC GTGAGGGTAA      500
   CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC      550
   TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG      600
   CTGACCGGTC TGACTATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
60  ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGGCC GGTACCGAAG      700

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TATCTGCACT	GTTGGGTCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCAACG	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACCT	CGACCAAAAC	800
GGTTCAATC	A				811

5

2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GC	GATGCTAT	TCC	ACGCGTT	TAC	GATGCGT	TG	AAACTGGT	TG	ATGTGGAC	50
TT	GACATTAG	AAG	TGCAACA	ACA	ACTGGGC	GAT	GGCGTAG	TG	CGTACCAT	100
25	TGCGATGGGT	AGT	ACCGATG	GTT	TGAAACG	CGG	CTTAGCC	GT	GAACAACA	150
CAG	GCGCACC	TAT	TACAGTG	CCT	GTTGGTA	AAG	CAACATT	GGG	TCGTATT	200
AT	GGACGTAT	TGG	TAATCC	TGT	TGATGAA	GC	AGGTCCAA	TT	GGTTCTGA	250
CCA	AACGCGT	GCT	ATTCACC	AAC	CAGCTCC	TAA	ATTTGAT	GA	ACTGTCTA	300
GCG	CAACCGA	ATT	GCTGGAA	AC	AGGCATCA	AAG	TGATTGA	CTT	GCTTTGC	350
30	CCATTTGCAA	AAG	GTGTA	AGT	AGTTTG	TTT	GGTGGTG	CAG	GTGGG	400
CA	AACTGTG	AAC	ATGATGG	AGT	TGATTAA	CA	ACATTGCC	AA	AGCGCACA	450
GT	GGTTTGTC	TGT	ATTTGCA	GGC	GTGGGTG	AAC	GTA	CG	AAGGTAAT	500
GAC	TTCTATC	ACG	AGATGAA	AG	ATTCTAAC	GT	GTTGGATA	AAG	TGCCAT	550
GGT	GTATGGT	CAA	ATGAATG	AAC	CTCCTGG	CA	ACCGTTTG	CG	CGTTGCAT	600
35	TGACTGGTTT	GT	CTATGGCA	GA	ACACTTCC	GT	GATGAAAA	AG	ACGAAAAT	650
GG	CAAAGGTC	GCG	ATGTATT	GTT	CTTTGTG	GAC	AACATCT	AT	CGCTACAC	700
ATT	TGGCAGGT	AC	GAAAGTAT	CGG	CATTGCT	GGG	TCGTATG	CC	CTCTGCGG	750
TAG	GTTATCA	AC	CAACATTG	GC	AGAAGAAA	TGG	GTCGTTT	GCA	AGAGCGT	800
40	ATTACTTCAA	CG	AAACAGG	TTC	GATTACT	T				831

2) INFORMATION FOR SEQ ID NO: 313

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

AT	GCCGTACC	ACG	CGTGTAC	GA	AGCCCTTG	AGG	TACAGAA	TGG	TAATGAA	50
50	GTTCTGGTGC	TG	GAAGTTCA	GC	AGCAGCTG	GGC	GGCGGTA	TCG	TACGTAC	100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCCGA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CCAAGGGCGG	TAAAGTTGGT	CTGTTCCGGC	GTGCGGGTGT	400
	AGGTAAAACT	GTAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*
- (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCCGA	250
10	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAAACC	GTAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
15	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

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10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT      50
   GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG      100
   CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC      150
   GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT      200
15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG      250
   AGCGTTGGGC GATTACCCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC      300
   TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC      350
   GTTTGCGAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
20 GGTACTACCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA      500
   CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG      550
   TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG      600
   ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT      650
   GCTGTTCTGC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT      700
25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG      750
   GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CAAAACGGG      800
   TTCTATCACT TCC                                     813

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30

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

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35 (A) LENGTH: 822 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

```

   GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA      50
   GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG      100
   CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA      150
50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCG      200
   TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG      250
   AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG      300
   TTCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT CGTAAGGGCG GTAAAGTAGG TCTGTTTCGGT GGTGCGGGCG      400
55 TAGGTAA AAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT      550
   CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT      600
   GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
50 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG      700

```

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGGTTCT	ATCACTTCCG	TA			822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAAC	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GCGGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTACTCGTGA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGFT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTACTG	CTGTTCGTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGCGGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAAACCGGT	TCTATCACCT	CCGTA		785

10

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAGATC	100
50 TCGAGACCC	AATCGAAGTT	CCGGTMMGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCAKCC	AGTMGACATG	AAAGGCGACA	TCGGTGAAGA	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTTCGCTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTGTTG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGGTTACTC	CGTGTGTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTCG	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTAAGTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GTTTCTATC					759

15

2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*

(B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTTCAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTGTCTG	GAAACCGGCA	TCAAAGTTAT	350
10	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAACCGT	600
15	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTAAGTGTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
50	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

2) INFORMATION FOR SEQ ID NO: 320

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*

(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

```

10  GCCGTACCGC  GCGTGTACGA  AGCCCTTGAG  GTACAGAATG  GTAATGAAGT      50
    GCTGGTGCTG  GAAGTTCAGC  AGCAGCTCGG  TGGCGGTATC  GTGCGTACCA     100
    TCGCCATGGG  TTCCTCCGAC  GGTCTGCGTC  GCGGTCTGGA  AGTTAAAGAT     150
    CTCGAGCACC  CGATCGAAGT  TCCGGTAGGT  AAAGCAACAC  TGGGTCGTAT     200
    CATGAACGTA  CTGGGTCACC  CGGTAGACAT  GAAAGGCGAC  ATCGGTGAAG     250
    AAGAGCGTTG  GGCTATCCAC  CGCGCTGCGC  CTTCTACGA  AGAGCTGTCC     300
15  AGCTCTCAGG  AACTGCTGGA  AACC GG TATC  AAAGTTATCG  ACCTGATGTG     350
    TCCGTTCCGG  AAGGGCGGTA  AAGTCGGTCT  GTTCGGCGGT  GCGGGTGTTG     400
    GTAAAACCGT  AAACATGATG  GAGCTGATCC  GTAACATCGC  GATCGAGCAC     450
    TCCGGTTACT  CTGTGTTTGC  GGGCGTAGGT  GAACGTACTC  GTGAGGGTAA     500
    CGACTTCTAC  CACGAAATGA  CCGACTCCAA  CGTTATCGAT  AAAGTATCCC     550
20  TGGTGTATGG  CCAGATGAAC  GAGCCGCCGG  GAAACCGTCT  GCGCGTTGCG     600
    CTGACCGGCC  TGACCATGGC  TGAGAAATTC  CGTGACGAAG  GTCGTGACGT     650
    ACTGCTGTTC  GTCGATAACA  TCTATCGTTA  CACCCTGGCC  GGTACTGAAG     700
    TATCTGCAC  GCTGGGTCGT  ATGCCTTCAG  CGGTAGGTTA  CCAGCCGACT     750
    CTGGCGGAAG  AGATGGGCGT  TCTGCAGGAA  CGTATCACCT  CCACCAAGAC     800
25  CGGTTCTATC                                810

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2) INFORMATION FOR SEQ ID NO: 321

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus acidophilus*

(B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

```

15  TCGATAAGAA  TTTACCTGAT  ATTAACAACG  CCTTACGTGT  AATCAAGTCC      50
    GAAGATGAAA  GCATCGTTCT  TGAAGTTACA  CTTGAACTCG  GTGATGGTGT     100
    TTTAAGAACA  ATCGCCATGG  AATCTACCGA  TGGTCTTCGT  CGTGGTATGA     150
    AAGTCGAAGA  TACTGGCGCT  CCAATTTTCA  TTCCAGTTGG  AGAAGACACT     200
    TTAGGTCGTG  TGTTTAACGT  TTTAGGACAG  CCTATTGATG  GTGGTCCAGC     250
30  CTTTCCAAAG  GATCACCCAC  GTGAGGGTAT  CCACAAGGAA  GCACCTAAAT     300
    ATGAAGATTT  AACTACTAGT  CGTGAAATTC  TTGAAACTGG  TATCAAGGTT     350
    ATCGACCTTC  TTGAACCATA  TGTTCGTGGT  GGTAAAGTTG  GTTTGTTTGG     400
    TGGTGCCGGT  GTTGGTAAAA  CTACTATTAT  TCAAGAATTA  ATTCACAACA     450
    TCGCTCAAGA  ACACGGTGGT  ATTTCCGTAT  TTACTGGTGT  TGGTGAAAGA     500
55  ACTCGTGAAG  GTAATGACCT  TTACTTTGAA  ATGAAAGCTT  CAGGCGTTTT     550
    AAGTAAGACT  GCCATGGTAT  TTGGTCAGAT  GAACGAGCCG  CCTGGTGCCA     600
    GAATGCGTGT  TGCATTAACC  GGTTTGACAC  TTGCTGAATA  CTTTAGAGAT     650
    GTTGAAGGTC  AAGACGTATT  GCTCTTTATT  GACAATATCT  TTAGATTTAC     700
    TCAGGCTGGT  TCAGAGGTAT  CTGCTTTGCT  TGGTCGTATG  CCAAGTGCCG     750
60  TAGGTTATCA  GCCAACTTTG  GCAACAGAAA  TGGGTCAATT  GCAGGAAAGA     800

```

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTTG 350
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCTG GTGGTGCCGG 400
 TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCGG TTATTCAAGT TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40 2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimonitii*
 (B) STRAIN: ATCC 33999

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTCCGC	AAGGGCGGTA	AAGTCGGCCT	GTTCGGCGGC	GCCGGCGTAG	400
5	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCGC	550
	TGGTATACCG	TCAGATGAAC	GAGCCGCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACTT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACTCTTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCAAC	300
	GCGAAGCTCC	AACTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCTTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGGTG	CCGGTGTGGG	TAAAACCGTT	CTAATTCAAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTT	TGTGTTTCGT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTCAAGC	GTTATTGAAA	AAACAGCGAT	GGTATTTCGGT	CAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTCGCT	TAACTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 828 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus lylae*
 (B) STRAIN: ATCC 27566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

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    CCCGCGTGGC GAGTTGCCGG CACTGTTCAC CGCGCTGACT GTCGAGGTCA      50
    CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC      100
10  GGCACAACT TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT      150
    CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG      200
    GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT      250
    GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC      300
    GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA      350
15  TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC      400
    CTGTTCCGGT GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT      450
    CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG      500
    GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG      550
    GGCCTTCTCC AGGACACCGC TCTTGTGTTT GGCCAGATGG ACGAGCCTCC      600
20  AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT      650
    TCCGCGATGT GCAGCACCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC      700
    CGTTTCACCC AGGCAGGTTT CGAGGTTTCC ACCCTCCTAG GCCGCATGCC      750
    TTCTGCCGTG GGTTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC      800
25  AGGAGCGTAT TACCTCCACA AAGGGTAA      828
  
```

2) INFORMATION FOR SEQ ID NO: 326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

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    GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
45  AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTTCGTT      100
    GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA      150
    AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG      200
    TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG      250
    AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG      300
50  GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT      350
    TTGCCCATTG GCTAAAGGGG GTAAAGTGGG TCTGTTTCGGT GGTGCGGGTG      400
    TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG      450
    CACTCAGGTT ATTCTGTATT CGCGGGTGTT GGTGAACGTA CTCGTGAAGG      500
    TAACGATTTT TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT      550
55  CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT      600
    GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG      700
    AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA      750
    ACGCTGGCGG AAGAGATGGG TGTTCGCAA GAACGTATCA CCTCGACTAA      800
50  GACCGGCTCT ATCACTTCCG TA      822
  
```

2) INFORMATION FOR SEQ ID NO: 327

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

20	CCGTGGCGAT	GTCCCCCAA	TCTTTGATGC	ACTTCATGTT	GATGGTACTG	50
	AAACCACCT	TGAAGTCAA	CAACAGTTAG	GTGATGGTGT	GGTGCGTACC	100
	ATTGCCATGG	GTTCTACCGA	AGGCTTAAAG	CGTGGCTTGC	CTGTCTCTAA	150
	TTCAGGTGCA	CCCATTTTCG	TACCACTCGG	TCAAGCAACA	CTGGGTCGCA	200
	TTATGGATGT	CCTAGGTCGC	CCAATCGATG	AAGCAGGTCC	GGTAAATGCT	250
25	GAACAAAAAT	GGTCCATTCA	TCGTGAAGCA	CCAAGTTATG	ATGAACAGTC	300
	AAATAGTACA	GAACCTTTTAG	AAACAGGCAT	CAAAGTGATT	GATTTGCTTT	350
	GTCCATTTGC	CAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTG	TGCTGGTGTG	400
	GGTAAGACCG	TTAACATGAT	GGAGCTTATC	AATAATATCG	CCCTAAAACA	450
	CTCAGGTCTG	TCGGTTTTTG	CTGGTGTGGG	TGAGCGTACT	CGTGAGGGTA	500
30	ATGACTTCTA	CCATGAAATG	CAAGAAGCAG	GCGTTGTTAA	TACCGAAGAT	550
	TTTACTCAGT	CAAAAGTTGC	CATGGTTTAT	GGTCAGATGA	ATGAGCCACC	600
	AGGAAACCGT	CTGCGTGTTG	CCTTAACTGG	TTTGACCATG	GCAGAGTATT	650
	TCCGTGATGA	AAAAGACGAA	GCAACGGGCA	AAGGCCGTGA	TGTTCTGCTG	700
	TTCGTTGATA	ATATTTATCG	TTACACATTG	GCAGGTACTG	AGGTATCAGC	750
35	ACTTTTAGGT	CGTATGCCAT	CTGCGGTAGG	TTATCAGCCG	ACTTTGGCCG	800
	AAGAGATGGG	CTTGCTACAA	GAGCGTATCA	CCTCCACCCA	ATCAGGCTCA	850
	ATTA					854

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

50	CCGTCAAAGC	GTACCAAGAA	TTTATGATGC	CTTAAAAGTT	GAAGGCACAG	50
	AAACTACATT	AGAAGTACAA	CAACAATTGG	GTGATGGTAT	CGTACGTACT	100
	ATTGCCATGG	GTTCTACTGA	AGGTCTAAAA	CGTGGTCTAC	CAGTTAGCAA	150
50	CACTGGCGCA	CCAATCTCTG	TACCTGTGGG	TAAAGGTACA	CTAGGTCGTA	200

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAACCTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTCG	TAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTG	CGCGGGTGTT	400
5	GGTAAAACCG	TTAACATGAT	GGAACCTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATTG	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAGA	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

2) INFORMATION FOR SEQ ID NO: 329

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTCTT	CAGGATGCAG	TACCGAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACATCG	CGCGAGAAGA	AAAATTGGTCT	ATTCACCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAACT	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCC	TTCGCGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGGTGC GG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTTCGAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAG	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTCGTTG	ATAACATCTA	CCGTTATACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGTTA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

2) INFORMATION FOR SEQ ID NO: 330

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea agglomerans*

(B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTAGTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTCACCG	CGCAGCCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTT	TGCTGTTCAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCGG	TACAGAAGTT	TCTGCACGTC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 808 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea dispersa*

(B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATTG	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTGCA	GGAACCTGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CGAAGGCGCG	TAAAGTCGGT	CTGTTGCGTG	GTGCGGGTGT	400
	AGGTAAACCC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
50	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

5 2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
(B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100
TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
AACCCAATTT CTGTTCCAGT GGGAACGAAA ACATTGGGTC GTATCATGAA 200
25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300
ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
TGCGAAAGGG GGTAAAGTAG GTTTATTCGG TGGTGCGGGT GTCGGTAAAA 400
CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGT TT 550
ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
GGCTTAACTA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCTTGCA 750
GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800
TATTA 805

10 2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCTG 100
TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
50 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCTG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTACTGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGCGGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAAACC	GGTTCAATCA	CTTCTGTA			828

15

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 25933

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	GTTCAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGCACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
10	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTTGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GGTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
15	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTCGTC	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

30

2) INFORMATION FOR SEQ ID NO: 335

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

	CCCTAAAGTA	TACGACGCTC	TTGAGGTTAT	GAATGGTAAA	GAGAAACTGG	50
10	TGCTAGAAAGT	TCAGCAACAG	TTAGGCGGTG	GTATCGTTTCG	TTGTATCGCA	100
	ATGGGTACAT	CAGACGTTTT	AAGCCGTGGC	TTAAAAGTTG	AAAACCTTAGG	150
	CCACCCAATT	GAAGTACCAG	TAGGTAAAGC	AACACTGGGA	CGTATCATGA	200
	ACGTTCTGGG	TACACCTATC	GATATGAAAG	GTGATATTGC	AACTGAAGAA	250
	CGTTGGTCTA	TTCACCGCGA	AGCGCCAACC	TATGAAGAGT	TATCAAGCTC	300
15	TCAAGAACTA	CTAGAAACCG	GTATCAAAGT	AATGGACTTA	ATCTGTCCGT	350
	TTGCTAAAGG	TGGTAAAGTA	GGTCTCTTCG	GTGGTGCGGG	TGTTGGTAAA	400
	ACAGTTAACA	TGATGGAATT	GATCCGTAAC	ATCGCGATTG	AGCACTCAGG	450
	TTATTCTGTA	TTTGCAGGTG	TTGGTGAGCG	TACTCGTGAG	GGTAACGACT	500
	TCTATCATGA	AATGACAGAT	TCTAACGTTT	TTGACAAAGT	ATCGTTAGTT	550
20	TATGGTCAGA	TGAATGAGCC	ACCAGGAAAC	CGTCTACGTG	TAGCACTGAC	600
	GGGTTTAACC	ATGGCGGAAA	AATTCCGTGA	TGAAGGCCGT	GACGTACTGT	650
	TATTCGTCGA	TAACATCTAT	CGTTACACCT	TAGCCGGTAC	CGAAGTATCA	700
	GCACTGTTAG	GCCGTATGCC	ATCAGCAGTA	GGTTACCAAC	CAACATTGGC	750
	TGAAGAGATG	GGTGTCTG	AAGAACGTAT	CACTTCAACC	AAAACAGGTT	800
25	CAATCACCTC	T				811

2) INFORMATION FOR SEQ ID NO: 336

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

15	TCAAGATAAC	GTACCAAAAG	TGTACGATGC	TCTTGAGGTT	ATTAACGGTA	50
	AAGAAAAACT	GGTGTGGAA	GTTCAACAAC	AGTTAGGTGG	TGGTGTGTC	100
	CGTTGTATCG	CAATGGGTAC	ATCAGATGGT	CTGAGCCGTG	GTTTAGAAGT	150
	TGTAAACTTA	GAGCACCAA	TGAAGTACC	AGTCGGTAAA	GCAACTCTGG	200
	GACGTATCAT	GAACGTTCTG	GGTGAACCAA	TCGACATGAA	AGGTGATATC	250
50	GGCGAAGAAG	AGCGCTGGTC	TATTCACCGT	GCTGCACCAA	GCTACGAAGA	300
	ATTAGCTAAC	TCAACTGAAC	TGCTGGAAAC	CGGTATCAAA	GTAATGGACT	350
	TAATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TAGGTCTGTT	CGGTGGTGCG	400
	GGTGTGGTA	AAACCGTAAA	CATGATGGAA	CTGATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TGTTGCTGG	TGTTGGTGAG	CGTACCCGTG	500
55	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ACTCAAACGT	TCTGGATAAA	550
	GTATCACTGG	TTTATGGCCA	GATGAACGAG	CCACCAGGAA	ACCGTCTGCG	600
	TGTTGCGCTG	ACTGGTCTGA	CTATGGCTGA	AAAATTCCGT	GACGAAGGTC	650
	GTGACGTACT	GCTGTTCTG	GACAACATTT	ATCGTTATAC	ACTGGCAGGT	700
	ACTGAAGTAT	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	750
50	ACCAACGCTG	GCGGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATTACCTCAA	800

5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
CGGTAAAGAA AACTGGTGC TGGAAAGTTCA GCAACAGTTA GGCGGTGGTG 100
TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
GGACTTAATC TGTCCATTCT CGAAAGGTGG TAAAGTTGGT CTGTTCCGGTG 400
GTGCGGGTGT TGGTAAACAA GTAAACATGA TGGAACTGAT CCGTAACATC 450
30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTTG GTGAGCGTAC 500
TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTG 700
35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

10 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
ACTGGTGTTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTT GTCCGTTGTA 100
TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTTC	400
5	GTAAAACAGT	AAACATGATG	GAACCTGATCC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTTCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTAAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	G TTCAGCAAC	AGTTAGGCGG	TGGTGTTCGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
10	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
15	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
50	CTAAGACAGG	TTCTATCAC				819

50

2) INFORMATION FOR SEQ ID NO: 340

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Psychrobacter phenylpyruvicus*

(B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

	AACCGCACTG	ACGTGCCTCA	AATTTATGAC	GCGTTAGTTG	TAGATGGTAC	50
10	CGAAACCACC	CTAGAAGTTC	AGCAGCAGCT	GGGCGATGGT	GTGGTACGTA	100
	CTATTGCAAT	GGGATCTACT	GAAGGTCTTA	AGCGTGGTTT	ACCAGTAACA	150
	AACACTGGTG	CCCCAATTAC	AGTTCCAGTA	GGTGATGCGA	CTTTAGGTCTG	200
	TATTATGGAC	GTTTTAGGTC	GTCCAATTGA	CGAACAAGGT	CCAGTTAATT	250
	CTGAAGACCA	TTGGTCAATC	CACCGTCAAG	CGCCATCATA	TGATGAGCAA	300
15	GCTAACAGTA	CTGACCTATT	AGAGACAGGT	ATTAAAGTAA	TTGACTTACT	350
	TTGTCCGTTC	GCTAAAGGGG	GTAAAGTTGG	TCTGTTCCGT	GGTGCCGGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAATTGA	TTAATAACAT	CGCTCTTAAG	450
	CACTCAGGTT	TATCAGTATT	CGCTGGTGTG	GGTGAGCGTA	CTCGTGAAGG	500
	TAACGACTTC	TACCACGAGA	TGCAAGAAGC	GGGTGTTGTT	GACGTTGAAA	550
20	ACTTCACCAA	CTCAAAAGTT	GCGATGGTTT	ATGGTCAGAT	GAATGAGCCA	600
	CCAGGTAACC	GTTTACGTGT	TGCGTTAACC	GGTCTGACTA	TGGCTGAGTA	650
	CTTCCGTGAT	CAAAAAGATG	AAAACGGTAA	AGGTAAAGAC	GTTCTATTAT	700
	TCGTTGATAA	CATCTACCGC	TACACGCTAG	CCGGTACTGA	AGTATCAGCA	750
	CTTCTAGGTC	GTATGCCATC	AGCAGTAGGT	TATCAGCCAA	CACTAGCGGA	800
25	AGAGATGGGT	GTACTACAAG	AGCGTATTAC	TTCAACTCAG	ACTGGTTCTA	850
	TTACTTC					907

30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rahnella aquatilis*

(B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

45	GTTCCCTCAG	GATGCAGTAC	CGAACGTGTA	CAATGCTCTT	GAGGTAGAAA	50
	ACGGTACCTC	CAAACCTGGT	CTGGAAGTTC	AGCAACAGTT	AGGCGGCGGC	100
	GTTGTTCGTT	GTATCGCAAT	GGGTACCTCA	GACGGCCTGC	GTCGCGGTCT	150
	GAAAGTGAAC	AACCTGGAAC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCGA	200
50	CTCTGGGTCG	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAAGGT	250
	GAAATCGGCG	AAGAAGAACG	TCGTGCTATT	CACCGTGCTG	CGCCTTCTTA	300
	TGAAGAGCTG	GCAAACCTCC	AGGAATTGCT	GGAAACCGGT	ATCAAAGTTA	350
	TGGACCTGAT	GTGTCCGTTT	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCCGT	400
	GTTGCGGGTG	TAGGTAAAAC	TGTGAACATG	ATGGAGCTGA	TCCGTAACAT	450
55	TGCGATCGAG	CACTCCGGTT	ATTCTGTGTT	TGCAGGCGTG	GGTGAACGTA	500
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACTGATTC	CAACGTTATC	550
	GACAAAGTTT	CCCTGGTGTA	TGGCCAGATG	AATGAGCCAC	CAGGTAACCG	600
	TCTGCGCGTT	GCACTGACCG	GCCTGACCAT	GGCGGAAAAA	TTCCGTGATG	650
	AAGGTCGTGA	CGTACTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	700
60	GCCGGTACCG	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	750

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCCGGTG 400
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASC CGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 55 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCCA	CGCTGGGTCTG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAACCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGCG	GTAAAGTCCG	TCTGTTCCGT	GGTGC GG GTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCGGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCTG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTCGACAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

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10  TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
    TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
    TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
    GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC      200
15  GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
    AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCTGC GCCGTCCTAC      300
    GAAGAGTTGT CAAACTCTCA GGAAGTGTCTG GAAACCGGTA TCAAAGTTAT      350
    CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCCGGTG      400
    GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
20  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
    ATAAAGTATC CCTGGTGTAT GGTGAGATGA ACGAGCCGCC GGGAAACCGT      600
    CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA      650
    AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
25  CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCCTT CGCGGTAGGT      750
    TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
    CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                      831

```

30 2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

```

    TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
    TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
    TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
50  GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC      200
    GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
    AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAT      300
    GAAGAGTTGT CAAACTCTCA GGAAGTGTCTG GAAACCGGTA TCAAAGTTAT      350
    CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCCGGTG      400
55  GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
    GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
    ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
    CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA      650
60  AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700

```

CCGGTACGGA	AGTTTCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
TATCAGCCAA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
CTCCACCAA	ACCGTTCTA	TCACCTCCG			829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 20 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

25	GCCGTACAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAGAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
30	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
35	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
40	CGGTTCTATC	ACCTCCG				817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGC	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTGG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTA	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTT					806

20

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
- (B) STRAIN: ATCC 43972

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCCGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
45	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTA	CTGTCGATAA	CATCTATCGT	TATACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 823 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500

	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	510
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTA CTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
5	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	CGCAGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAA	ACCGGTTCTA	TCACCTCCGT	A		831

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Virchow
25 (B) STRAIN: ATCC 51955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
30	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTCTCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
40	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
45	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 353

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Serratia ficaria*
(B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTT	GCCAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCGCG	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: ATCC 29844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACCGA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTTCGGT	GGTGCTGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTACTG	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTGCTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCGCG	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

```

15  GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA      50
    TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT      100
    GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA      150
    GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CTCTGGGCCG      200
20  TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG      250
    AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTG      300
    GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT      350
    CTGCCCCGTT GCCAAGGGTG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG      400
    TTGGTAA AACGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
25  CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG      500
    TAACGACTTC TACCACGAAA TGAACGACTC CAACGTA CTG      550
    CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT      600
    GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA      650
    CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG      700
30  AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA      750
    ACGCTGGCGG AAGAGATGGG TGTCTGCAA GAACGTATCA CCTCTACCAA      800
    GACTGGTTCA ATCACCTCCG TA      822
  
```

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

```

    ATGCCGTACC AAAAGTGATC AATGCTCTTG AGGTAGAAAA CGGTACCGAG      50
    AAGCTGGTGC TGAAGATTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG      100
    TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG      150
55  ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT      200
    ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA      250
    AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT      300
    CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT      350
    TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCTGGTGT      400
60  TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC      450
  
```

ACTCCGGTTA	TTCCGTGTTT	GCAGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
5 GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
AGTGTTCCGA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
ACCGGTTCTA	TCACTTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
CCGAAAAACT	GGTGTGGA	GTTCAGCAAC	AGCTGGGCGG	TGGCGTGTT	100
30 CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
GGCGAAGAAG	AGCGTTGGGC	GATTACCCGC	GCGGCGCCAA	GCTACGAAGA	300
GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
35 TGATTTGTCC	GTTCGCCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
40 CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
GTGACGTTCT	GCTGTTCGTT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
ACCGAAGTGT	CCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
CCAAG					805

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2) INFORMATION FOR SEQ ID NO: 358

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 60 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	AACTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTGGTTCGTT	100
	GTATCGCTAT	GGGCACCTCC	GACGGTTTGC	GTCGCGGCCT	GAAAGTGAAC	150
	GATCTGCAAC	ACCCAATCGA	AGTCCCGGTT	GGCAAGGCAA	CGCTGGGTCTG	200
	TATCATGAAC	GTATTGGGTC	AACCAATCGA	CATGAAAGGC	GACATCGGCG	250
	AAGAAGAGCG	TTGGGCGGATT	CACCGCGCGG	CGCCAAGCTA	CGAAGAAGTG	300
10	TCCAACCTCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTTA	TGGACCTGAT	350
	CTGCCCCGTTT	GCCAAGGGTG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCAGTGTT	TGCGGGCGTG	GGTGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTACTG	GACAAGGTTT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CGGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCCGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCTGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 359

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia plymuthica*

(B) STRAIN: ATCC 183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

40	GTGTACAACG	CTCTTGAGGT	AGAAAACGGT	GCCAATAAGC	TGGTGCTGGA	50
	AGTTCAGCAA	CAGCTGGGCG	GTGGCGTGGT	TCGCTGTATC	GCGATGGGGA	100
	CCTCTGATGG	TCTGCGTCGC	GGTCTGAAAG	TGATCGACCT	GGATCACCCG	150
	ATTGAAGTAC	CGGTAGGTAA	AGCTACCCTG	GGCCGTATCA	TGAACGTATT	200
	GGGTGAACCA	ATCGACATGA	AAGGCGACAT	CGGCGAAGAA	GAACGTTGGG	250
45	CAATTCACCG	TCCAGCGCCA	AGCTACGAAG	ATTTGGCCAA	CTCCAGGAT	300
	CTGCTGGAAA	CCGGTATCAA	GGTTATGGAC	CTGATCTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTGGGTCTGT	TCGGCGGTGC	GGGCGTGGGT	AAAACCGTAA	400
	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAACACTC	CGGTTATTCC	450
	GTGTTTGCGG	GCGTGGGTGA	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
50	CGAAATGAAC	GACTCCAACG	TACTGGACAA	AGTATCCCTG	GTTTACGGCC	550
	AGATGAACGA	GCCACCGGGT	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCGG	AGAAATTCCG	TGACGAAGGC	CGCGACGTTT	TGCTGTTCTG	650
	TGATAACATC	TACCGTTATA	CCCTGGCCGG	TACCGAAGTG	TCCGCACTTC	700
	TGGGCCGTAT	GCCATCTGCG	GTAGGTTATC	AGCCAACGCT	GGCGGAAGAG	750
55	ATGGGCGTTC	TGCAAGAACG	TATCACCTCT	ACCAAGACCG	GTTCTATCAC	800
	CTCCG					805

60 2) INFORMATION FOR SEQ ID NO: 360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

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15  TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA      50
    CGGTAACGAA AAAGTGGTGC TGGAAAGTTCA GCAGCAGCTG GGC GGCGGCGG 100
    TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
    AAAGTTAACG ACCTCGAGCA CCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
20  GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
    ACATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCAAGCTAC 300
    GAAGAGCTGT CCAGCTCCCA AGAGTGTCTG GAAACCGGTA TCAAGGTAAT 350
    GGACCTGATC TGCCCGTTTC CCAAGGGTGG TAAAGTTGGT CTGTTCTGGT 400
    GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
25  GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
    ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
    CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
    AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
30  CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT 750
    TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
    CTCGACCAAG ACCGGTTCAA TCACCTCCGT A      831
  
```

2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCDC D7172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

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55  CCGTAAACAT GATGGAAGT ATCCGTAAAC TCGCCATCGA GCACAGCGGT      50
    TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 100
    CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
    ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
    GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
    GTTCGTCGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
    CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT 350
    GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTT 400
60  GATCAC      406
  
```

2) INFORMATION FOR SEQ ID NO: 362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	50
	TGTAATGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ACCTCGAACA	CCCGATCGAA	GTCCCAGGTAG	GTAAAGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	250
25	AGATCGGTGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAACCTCTCA	GGAAC TGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
30	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ACAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
35	TATCAGCCGA	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACTGGTTCTA	TCACCTCCGT	A		831

2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55	GCCGTACCGC	GCGTGTACGA	TGCTCTTGCG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCAATGGG	TTCTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
60	CATGAACGTA	CTGGGTGAAC	CGGTGCACAT	GAAAGGCGAG	ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTCATTG	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CG					802

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2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
35	ACCTCGAACA	CCCGATCGAA	GTCCCAGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTA	GGAAC TGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
40	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
45	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACTGGTTCTA	TCACCTCCG				819

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2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella sonnei*

(B) STRAIN: ATCC 29930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

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GTACCGCGCG	TGTACGATGC	TCTTGAGGTG	CAAAATGGTA	ATGAGCGTCT	50
GGTGCTGGAA	GTTACAGCAGC	AGCTCGGCGG	CGGTATCGTG	CGTACCATCG	100
CAATGGGTTC	CTCCGACGGT	CTGCGTCGCG	GTCTGGATGT	AAAAGACCTC	150
GAACACCCGA	TCGAAGTCCC	GGTAGGTAAA	GCGACTCTGG	GCCGTATCAT	200
GAACGTACTG	GGTGAACCGG	TCGACATGAA	AGGCGAGATC	GGTGAAGAAG	250
AGCGTTGGGC	GATTCACCGC	GCAGCACCTT	CCTACGAAGA	GCTGTCAAAC	300
TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAA	GTTATCGACC	TGATGTGTCC	350
GTTCGCTAAG	GGCGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	400
AAACCGTAAA	CATGATGGAG	CTCATTCGTA	ACATCGCGAT	CGAGCACTCC	450
GGTTACTCTG	TGTTTGCGGG	CGTAGGTGAA	CGTACTCGTG	AGGGTAACGA	500
CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TATCGACAAA	GTATCCCTGG	550
TGTATGGCCA	GATGAACGAG	CCGCCGGGAA	ACCGTCTGCG	CGTTGCTCTG	600
ACCGGTCTGA	CCATGGCTGA	GAAATTCCGT	GACGAAGGTC	GTGACGTTCT	650
GCTGTTCGTT	GACAACATCT	ATCGTTACAC	CCTGGCCGGT	ACGGAAGTAT	700
CCGCACTGCT	GGGCCGTATG	CCTTCAGCGG	TAGGTTATCA	GCCGACCCTG	750
GCGGAAGAGA	TGGGCGTTCT	GCAGGAACGT	ATCACCTCCA	CCAAAACCTG	800
TT					802

2) INFORMATION FOR SEQ ID NO: 366

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

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TAACGCCTTG	GTTATTGATG	TGCCTAAAGA	AGAAGGTACA	ATACAACTAA	50
CATTAGAAGT	TGCGCTGCAA	TTAGGTGACG	ACGTTGTTCG	TACAATTGCG	100
ATGGATTCAA	CTGATGGTGT	CCAAAGAGGC	ATGGATGTAA	AAGATACAGG	150
CAAAGAAATT	AGTGTAACCTG	TTGGTGATGA	AACATTAGGT	CGTGTATTTA	200
ATGTACTAGG	TGAAACAATT	GACCTTAAAG	AAGAAATTAG	TGATTCTGTT	250
CGCCGCGATC	CTATCCATCG	TCAAGCACCA	GCATTGATG	AACTTTCAAC	300
AGAAGTTCAA	ATTTTAGAAA	CAGGTATTAA	AGTAGTAGAT	TTACTAGCAC	350
CTTATATTAA	AGGTGGTAAA	ATCGGATTGT	TCGGTGGTGC	CGGTGTAGGT	400
AAAACAGTAT	TAATCCAAGA	ATTAATTAAC	AACATCGCTC	AAGAGCACGG	450
TGGTATTTCT	GTATTCGCCG	GTGTAGGTGA	ACGTACTCGT	GAAGGTAACG	500
ATTTATACTT	CGAAATGAGT	GATAGTGGTG	TAATTAAGAA	AACAGCCATG	550
GTATTCGGGC	AAATGAATGA	GCCACCTGGT	GCACGTATGC	GTGTTGCATT	600
ATCTGGTTTA	ACAATGGCTG	AATATTTCCG	TGACGAACAA	GGTCAAGACG	650
TATTATTATT	CATCGATAAC	ATTTTCAGAT	TTACACAAGC	TGGTTCTGAG	700
GTATCTGCAT	TATTAGGTCG	TATGCCTTCT	GCAGTAGGTT	ACCAACCAAC	750
ACTTGCTACT	GAAATGGGAC	AATTACAAGA	ACGTA		785

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG	AAGTGCCTAA	TATTAATAAC	GCCTTAGTAC	TCGATGTTGA	50
AAGAGAAGAC	GGAACAGTGT	CTTTAACTTT	AGAAGTAGCT	TTACAATTAG	100
GCGATGACGT	TGTTTCGTACC	ATTGCAATGG	ATTCAACTGA	TGGTGTTAAA	150
CGTGGTAAACG	AAGTCAAAGA	TACTGGTAAT	AGCATTAGCG	TACCAGTCGG	200
AGACGAAACT	TTAGGACGTG	TCTTCAACGT	TCTAGGTGAA	ACAATTGATT	250
TAGAAGATAA	ACTTGATGAT	TCTGCGCGAC	GTGACCCTAT	ACATAGAGAA	300
GCGCCAGCGT	TTGATCAATT	ATCAACTCAA	GTTGAAATTT	TAGAAACAGG	350
AATTAAAGTT	GTTGACTTAT	TAGCACCTTA	TATTAAAGGT	GGTAAAGTTG	400
GACTCTTCGG	TGGTGCCGGT	GTTGGTAAAA	CCGTTTTAAT	CCAAGAATTA	450
ATCAACAACA	TCGCTCAAGA	ACACGGTGGT	ATTTTCAGTCT	TTGCCGGTGT	500
AGGTGAACGT	ACACGTGAAG	GTAACGACTT	GTACTATGAA	ATGAGCGACA	550
GTGGTGTAAT	CAAGAAAACA	GCCATGGTCT	TCGGACAAAT	GAACGAACCA	600
CCTGGCGCAC	GTATGCGTGT	TGCTTTATCT	GGTTTAACAA	TGGCTGAATA	650
TTTCCGTGAT	GAACAAGGAC	AAGACGTATT	GTTATTTCATC	GACAATATTT	700
TCCGTTTCAC	ACAAGCCGGT	TCAGAAGTTT	CTGCCTTACT	AGGTCGTTTA	750
CCATCAGCCG	TTGGTTATCA	ACCTACATTA	GCAACAGAAA	TGGGACAATT	800
ACAAGAACGT	ATTACTTCAA	CAACAAAAGG	ATCAGTTACT	TCA	843

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA	TAATGAAGTT	CCTGATATTA	ACAATGCCTT	ACACATCGAA	50
GTTCCTAAAG	AAGATAGCAC	ACTTCATTTA	ACTTTAGAAG	TTGCACTTCA	100
ATTAGGTGAC	GATGTAGTAC	GTACAATCGC	AATGGACTCA	ACTGACGGCG	150
TTCAAAGAGG	TATGGAAGTT	AAAGATACAG	GTAAAGATAT	TAGCGTACCT	200
GTTGGTGATG	CAACTTTAGG	AAGAGTATTT	AACGTATTAG	GAGAAACAAT	250
CGATTTAGAT	GAAAAGATTG	ATGATTTCAGT	ACGTCGTGAT	CCTATTTCATA	300
GACAGGCACC	TGGCTTCGAT	GAATTATCTA	CTAAAGTAGA	AATCTTAGAA	350

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTGG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTT	AGTATTCGCC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCTT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTTCG	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAACA	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

```

5  AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT      50
   AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG      100
   CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA      150
   GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTCTAG GAAGAGTGTT      200
10  TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG      250
   TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA      300
   ACAAAGTAG  AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC      350
   ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG      400
   GTAAAACCGT ACTAATCCAA GAACCTATTA ATAACATCGC TCAAGAACAC      450
15  GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA      500
   TGATCTTTAC TATGAAATGA GTGACAGTGG TGTTATCAAG AAAACTGCAA      550
   TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA      600
   TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA      650
   TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG      700
20  AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT      750
   ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA      787

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2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

```

40  GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA      50
   TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAATA GGTGATGACG      100
   TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTC ACGTGGTATG      150
   GAAGTTCAGA ACACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC      200
45  TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA      250
   AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC      300
   TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT      350
   TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG      400
   GTGGTGCCGG TGTTGGTAAA ACCGTTTTTAA TCCAAGAATT GATTAATAAT      450
50  ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG      500
   TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA      550
   TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA      600
   CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA      650
   TGAACAAGGA CAAGACGTTT TGTTATTCAT CGATAACATT TTCAGATTTA      700
55  CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT      750
   GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG      800
   TATTACATCA ACGAATAAAG GTTCAGTAAC      830

```

60

2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

TCGAACATAA	TGAAGTCCCT	GAAATTAATA	ATGCCCTAAT	TATTGAAGTA	50
CCCAAAAATG	ATGGCACATT	TAAATTAACA	TTAGAAGTTG	CATTGCAACT	100
AGGTGATGAT	GTTGTTCGTA	CTATTGCAAT	GGATTCAACT	GATGGTGTTT	150
AACGTGGTAT	GCAAGTTGTG	AATACTGGTA	AAGATATTAG	TGTTCCCTGTA	200
GGTGAAGAAA	CACTTGGACG	TGTGTTTAAC	GTTTTAGGAG	AAACAATAGA	250
TTTAAACGAA	AAAATAGATA	GTTCTGTTAG	ACGTGATCCA	ATTCATCGTC	300
GTCAACCTAA	TTTTGATGAA	TTATCTACTG	AAGTAGAAAT	TCTTGAAACA	350
GGTATTAAAG	TTGTAGACTT	ATTAGCACCT	TATATTAAAG	GTGGTAAGAT	400
TGGTTTATTC	GGTGGTGCCG	GCGTAGGTAA	AACTGTATTA	ATTCAAGAAT	450
TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTCGCTGGT	500
GTAGGTGAAC	GTACTCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

TCGAACATAA	TGAAGTCCCT	GAAATTAATA	ATGCCCTAAT	TATTGAAGTA	50
CCCAAAAATG	ATGGCACATT	CAAATTAACA	TTAGAAGTTG	CATTGCAACT	100
AGGTGATGAT	GTTGTTCGTA	CTATTGCAAT	GGATTCAACT	GATGGTGTTT	150
AACGTGGTAT	GCAAGTTGTG	AATACTGGTA	AAGATATTAG	TGTTCCCTGTA	200
GGTGAAGAAA	CACTTGGACG	TGTGTTTAAC	GTTTTAGGAG	AAACAATAGA	250
TTTAAACGAA	AAAATAGATA	GTTCTGTTAG	ACGTGATCCA	ATTCATCGTC	300
GTCAACCTAA	TTTTGATGAA	TTATCTACTG	AAGTAGAAAT	TCTTGAAACA	350
GGTATTAAAG	TTGTAGACTT	ATTAGCACCT	TATATTAAAG	GTGGTAAGAT	400

	TGGTTTATTC	GGTGGTGCCG	GCGTAGGTAA	AACTGTATTA	ATTCAAGAAT	450
	TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTGCTGGT	500
	GTAGGTGAAC	GTACTCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
5	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

2) INFORMATION FOR SEQ ID NO: 374

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

	ATAATGAAGT	GCCTGAAATA	AATAATGCGC	TCATTGTTGA	AATTCCTAAA	50
30	AGTGATACAA	CAATCAGTTT	AACACTTGAA	GTTGCTTTGC	AATTAGGTGA	100
	CGATGTTGTA	CGTACTATTG	CAATGGATTG	AACTGATGGC	GTTCAACGTG	150
	GTATGGAAGT	TCAAAACACA	GGTAAAGACA	TCAGTGTACC	TGTTGGAGAT	200
	GAAACATTAG	GAAGAGTATT	TAACGTTTTA	GGAGAATCTA	TTGATTTAGA	250
	AGAAAAGCTA	GATGACTCTG	TGCGTAGAGA	TCCAATTCAT	AGACTAGCAC	300
35	CTAAATTTGA	TGAATTATCT	ACAGAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTTGTTG	ATTTATTAGC	ACCATATATT	AAAGGTGGTA	AAGTTGGATT	400
	GTTTGGTGGT	GCCGGAGTAG	GTAAAACGGT	ATTAATTCAA	GAATTAATCA	450
	ACAATATTGC	TCAAGAACAT	GGTGGTATTT	CTGTGTTTGC	CGGAGTAGGT	500
	GAACGTACAC	GTGAAGGTAA	TGACTTATAT	TATGAAATGA	GCGATAGTGG	550
40	CGTAATTAAG	AAAACAGCGA	TGGTATTTGG	CCAAATGAAT	GAACCACCTG	600
	GTGCACGTAT	GAGAGTTGCG	TTATCTGCCT	TAACAATGGC	TGAATATTTT	650
	CGTGACGAGC	AAGGACAAGA	CGTATTGCTG	TTTATCGATA	ATATATTCCG	700
	TTTTACACAA	GCAGGTTTCA	AAGTATCTGC	ATTACTTGG	CGTATGCCAT	750
	CTGCCGTTGG	TTATCAACCA	ACATTGGCTA	CAGAAATGGG	ACAATTGCAA	800
45	GAAAGAATTA	CATCTACAAA	TAAAGGTTCT	GTAAC		835

2) INFORMATION FOR SEQ ID NO: 375

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

5	GAGCACAATG	AAGTTCCAGA	AATTAACAAT	GCCTTAGTCG	TAGACGTTGA	50
	AAGAGATGAA	GGTACAGTAT	CTCTTACATT	AGAAGTGGCA	TTACAACCTG	100
	GCGATGATGT	CGTACGTACA	ATTGCAATGG	ATTCTACTGA	TGGTGTAAAA	150
	CGTGGTACAG	AAGTTCGAGA	TAGCGGAGAT	AGCATCAGTG	TTCCAGTTGG	200
	TGATGCTACG	TTAGGACGTG	TGTTTAATGT	TCTTGGTGAT	ACAATTGACT	250
10	TAGACGAGAA	GCTTGATACT	TCTGTCAAAC	GTGATCCAAT	TCATAGAGAA	300
	GCACCTGCAT	TCGATCAATT	ATCAACAAAA	GTTGAAATCT	TAGAAACAGG	350
	TATTAAAGTA	ATTGATTTAC	TTGCACCATA	TATTAAAGGT	GGTAAAATCG	400
	GTTTATTCGG	TGGCGCTGGT	GTAGGTAAAA	CAGTATTAAT	TCAAGAATTA	450
	ATTAATAATA	TAGCTCAAGA	ACATGGTGGT	ATTTCAGTAT	TTGCCGGCGT	500
15	AGGTGAACGT	ACGCGTGAAG	GTAATGACTT	ATACTACGAA	ATGAGTGATA	550
	GTGGTGTTAT	TAAGAAAACA	GCTATGGTCT	TCGGACAAAT	GAATGAGCCA	600
	CCTGGTGCGC	GTATGCGTGT	TGCTTTATCA	GGCTTAACAA	TGGCTGAACA	650
	CTTCCGTGAT	GTACAAGGAC	AAGATGTTTT	ACTATTTATT	GATAACATAT	700
	TCAGATTTAC	GCAAGCTGGT	TCAGAAAGTAT	CAGCACTATT	AGGTCGTATG	750
20	CCATCAGCCG	TTGGTTATCA	ACCTACCCTT	GCTACTGAAA	TGGGTCAATT	800
	ACAAGAACGT	ATTACATCAA	CAACTAAAGG	ATCTGTAACG	TC	842

25 2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 842 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus simulans</i>
	(B)	STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

40	TGATGAACTG	CCTAAGATTA	ATAACGCATT	AGTGCTAGAT	GTACCTAAGA	50
	AAGATGGCAC	GACTGAATCT	CTTACATTAG	AAGTAGCACT	TGAATTAGGC	100
	GACGACGTAG	TTAGAACTAT	CGCCATGGAC	TCTACAGACG	GAATTAAACG	150
	TGGTGACGAC	GTTAAAGACA	CTGGTCGTCC	AATCAGTGTA	CCTGTCGGTG	200
45	AAGATACGTT	AGGAAGAGTA	TTTAACGTTT	TAGGTGATCC	AATCGATAAT	250
	GATGGACCGA	TTTCTGAATC	AGTTCCACGT	GAACCAATTC	ATAGACAACC	300
	ACCTAAATTT	GATGAATTAT	CAACAAAAGT	TGAACTACTT	GAAACTGGTA	350
	TCAAAGTAGT	AGACTTATTA	GCACCATATA	TCAAAGGTGG	TAAAGTTGGT	400
	TTATTCGGTG	GTGCCGGAGT	AGGTAAAAC	GTATTAATCC	AAGAATTAAT	450
50	TAATAACATC	GCTCAAGAAC	ACGGCGGTAT	TTCAGTATTC	GCAGGTGTTG	500
	GTGAACGTAC	ACGTGAAGGT	AACGACTTGT	ACTTCGAAAT	GAGCGACAGT	550
	GGTGTTATCA	AGAAAACAGC	GATGGTATTC	GGACAAATGA	ACGAACCACC	600
	TGGTGCACGT	ATGCGTGTAG	CTTTATCAGG	TTTAACAATG	GCTGAATACT	650
	TCCGTGATGT	TAAAGGACAA	GACGTTCTTT	TATTCATCGA	TAACATTTTC	700
55	CGCTTCACAC	AAGCAGGTTT	TGAGGTATCA	GCATTGCTTG	GCCGTATGCC	750
	ATCAGCCGTT	GGTTACCAAC	CAACATTGGC	AACAGAAATG	GGTCAATTAC	800
	AAGAACGTAT	CACTTCTACA	ATGAAAGGTT	CTATCACATC	TA	842

60

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

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CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA      50
AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG      100
ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA      150
GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA      200
TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG      250
AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA      300
CCAGGTTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT      350
TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC      400
TATTCGGTGG TGCCGGAGTA GGTAACACCG TTTTAATCCA AGAATTAATT      450
AACAAATATT CACAAGAACA TGGTGGTATT TCAGTATTCG CGGGTGTAGG      500
TGAACGTACT CGTGAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG      550
GTGTAATTAA GAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT      600
GGCGCACGTA TCGGTGTAGC TTTATCTGGT TTAACATATG CTGAATACTT      650
CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA      700
GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT      750
TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA      800
AGAACGAATT ACATCTACAA ATAAAGGTTC TGTAACATCT A              841

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2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

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TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA      50
CAAAGACAGT GAGAAAAAAC ATAAAATCGT TCTTGAAGTA GCTCTTGAAC      100
TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG      150
ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT      200
TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG      250
ATCTTGAAGA ACCATTGGA GAAGATGCAG AACGTCACCC CATTGATAAG      300
AGTGCCCCAA CTTTGTGATG ATTATCAACG TCAACAGAAA TCCTTGAAAC      350
AGGGATTAAA GTTATCGACC TACTTGCCCC TTAATAAAA GGAGGGAAGG      400

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	TTGGACTTTT	CGGTGGTGCC	GGAGTTGGTA	AGACCGTTCT	TATCCAAGAG	450
	TTGATTCATA	ACATTGCTCA	AGAGCATGGT	GGTATTTCAG	TATTTACCGG	500
	AGTTGGTGAA	CGTACACGTG	AAGGTAATGA	CCTCTATTGG	GAAATGAAAG	550
	AATCAGGCGT	TATTGAAAAA	ACAGCTATGG	TATTTGGTCA	GATGAATGAG	600
5	CCACCTGGTG	CACGTATGCG	TGTAGCCCTT	ACTGGTTTGA	CAATCGCTGA	650
	ATATTTCCGT	GATGTTGAAG	GACAGGACGT	GCTTCTCTTT	ATTGATAACA	700
	TTTTTCGTTT	CACACAAGCA	GGTTCGAAG	TTTCAGCTCT	TCTTGGACGT	750
	ATGCCATCAG	CCGTTGGTTA	TCAACCAACC	TTGGCAACTG	AAATGGGTCA	800
	ATTGCAAGAA	CGTATCACGT	CAACTAAAAA	AGGTTCTGTT	ACATCA	846

2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

25 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
30	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTA	CTCTTGAAGT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCGAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCAG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
40	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
45	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

2) INFORMATION FOR SEQ ID NO: 380

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Streptococcus agalactiae*

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

5	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAAC	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
10	TCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACT	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCACT	ATTTACTGGT	500
15	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GTTTCTGTTA	CCTCAA	846

25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 845 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus agalactiae</i>
	(B)	STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

40	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAAC	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GTGCAATTAG	TGTGCCGGTT	200
45	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	ATTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
50	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCACT	ATTTACTGGT	500
	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
55	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GTTTCTGTTA	CCTCA	845

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2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

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TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC      100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA      750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTA CATCA          845

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2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

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TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC      100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400

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	TGGACTTTTC	GGTGGTGACG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTA CTCTGTA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
5	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CATCA	845

2) INFORMATION FOR SEQ ID NO: 384

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

	TTGCTAGTGG	GGACAAACTT	CCAGAGATTA	ATAATGCATT	GATTGTTTAT	50
30	AAAGATAGTG	ATAAAAAGCA	AAAAATCGTC	CTTGAAGTTG	CTCTGGAAGT	100
	TGGTGACGGT	ATGGTGCGAA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGGTT	AGAAGTTCTT	GACACTGGTC	GTGCGATTAG	TGTACCAGTA	200
	GGTAAAGAAA	CTTTGGGACG	CGTCTTTAAT	GTA CTTGAG	AAACCATTGA	250
	CTTGGAAGAA	CCATTTGCAG	AAGACGTTGA	CCGTCAGCCA	ATCCATAAAA	300
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	TCTTGAAAGT	350
	GGTATCAAGG	TAATTGACCT	TCTTGCCCCCT	TACCTTAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGGGGTGCCG	GAGTTGGTAA	GACTGTCCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCCCAA	GAACACGGAG	GTATTTTCAGT	ATTTACCGGT	500
	GTTGGTGAGC	GAACACGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAAGA	550
40	ATCAGGCGTT	ATTGAGAAAA	CTGCCATGGT	TTTTGGTCAG	ATGAATGAGC	600
	CGCCTGGGGC	ACGTATGCGT	GTA GCCCTTA	CTGGTTTAAC	CATTGCTGAG	650
	TATTTCCGTG	ATGTAGAAGG	CCAAGATGTT	TTGCTCTTTA	TTGATAATAT	700
	CTTCCGTTTC	ACTCAGGCAG	GTTCAGAAGT	ATCAGCCCTC	TTAGGCCGTA	750
	TGCCTTCTGC	TGTTGGTTAC	CAACCGACCC	TTGCTACTGA	AATGGGACAA	800
45	TTGCAAGAAC	GTATTACGTC	AACTCAAAAA	GGATCTGTTA	CTTCT	845

2) INFORMATION FOR SEQ ID NO: 385

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

5	TTGCGAGTGG	GGACAAACTA	CCAGAGATTA	ATAATGCGTT	GATAGTTTAT	50
	AAAGATGGCG	ATAAAAAGCA	AAAAATCGTT	CTCGAGGTTG	CCCTAGAGCT	100
	TGGAGACGGT	ATGGTACGTA	CAATTGCTAT	GGAATCAACC	GATGGGCTTA	150
	CACGTGGATT	AGAGGTTCTT	GATACTGGTC	GTGCCATTAG	TGTACCAGTT	200
	GGTAAAGAGA	CTCTAGGTCG	TGTTTTCAAC	GTTCTTGGTG	AAACCATCGA	250
10	CCTAGAAGCA	CCATTTGCAG	ATGATGTTAA	TCGTGAACCG	ATCCATAAAA	300
	AAGCACCAGC	CTTTGATGAA	TTGTCAACAT	CATCAGAAAT	TCTTGAAACA	350
	GGTATCAAGG	TTATTGACCT	GCTTGCCCCCT	TACTTAAAGG	GTGGTAAGGT	400
	CGGTCTTTTC	GGTGGTGCCG	GAGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCTCAA	GAGCATGGTG	GGATCTCGGT	ATTTACCGGT	500
15	GTTGGTGAGC	GTACGCGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAGGA	550
	ATCAGGCGTT	ATTGAAAAAA	CAGCCATGGT	TTTTGGTCAG	ATGAATGAAC	600
	CACCAGGAGC	CCGTATGCGT	GTTGCCTTGA	CCGGCTTGAC	AATTGCTGAA	650
	TATTTCCGCG	ATGTTGAAGG	CCAAGACGTC	CTGCTCTTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCAG	GCTCAGAGGT	ATCAGCCCTT	CTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAC	CAGCCAACAC	TTGCCACTGA	AATGGGACAA	800
	TTGCAAGAGC	GTATCACCTC	AACGAAAAAA	GGCTCTGTTA	CCTCTA	846

25 2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 846 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus anginosus</i>
	(B)	STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

40	TTGCAGCTGG	TGATAAATTA	CCTGAGATAA	ATAATGCACT	TGTAGTCTAT	50
	AAAAATGACG	AAAATAAATC	AAAAATCGTC	CTTGAAGTAG	CTCTTGAGCT	100
	TGGTGATGGA	GTGGTTCGAA	CTATTGCCAT	GGAATCCACT	GATGGGTTGA	150
	CTCGTGGCAT	GGAAGTTCTA	GATACTGGTC	GACCAATTTT	TGTTCCAGTT	200
45	GGGAAAGAAA	CACTTGGTCG	CGTCTTTAAC	GTTTTAGGCG	ATACCATTGA	250
	TTTGGAATACT	CCATTCGGCG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCTCCAAC	TTTTGATGAG	TTATCTACTT	CATCAGAAAT	CTTAGAAACA	350
	GGAATAAAGG	TTATTGACCT	TTAGCCCCC	TACCTCAAAG	GTGGGAAAGT	400
	CGGCCTCTTC	GGTGGTGCTG	GCGTTGGGAA	AACTGTCTTG	ATTCAAGAGT	450
50	TGATTCATAA	TATCGCCCAA	GAACACGGCG	GGATTTTCACT	CTTTACTGGT	500
	GTTGGGGAAC	GAACCTGTGA	AGGGAATGAC	CTGTACTGGG	AAATGAAAGA	550
	ATCTGGTGTT	ATCGAAAAGA	CGGCTATGGT	CTTTGGGCAA	ATGAATGAAC	600
	CGCCTGGAGC	ACGTATGCGT	GTAGCTTTGA	CTGGGTTAAC	GATTGCAGAG	650
	TATTTCCGTG	ATGTGGAAGG	TCAAGATGTT	CTTTTGTTTA	TTGATAATAT	700
55	TTTCCGTTTC	ACTCAAGCTG	GTTCTGAAGT	GTCAGCCCTT	CTTGGTCGTA	750
	TGCCATCAGC	TGTTGGTTAC	CAACCAACCT	TGGCTACTGA	AATGGGGCAA	800
	TTACAAGAAC	GTATTACATC	AACGAAAAAA	GGTTCTGTTA	CCTCAA	846

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2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

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GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC      50
TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG      100
GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT      150
CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG      200
TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT      250
TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA      300
GCACCAACTT TCGATGAATT GTCAACACTCT ACTGAAATCC TTGAAACAGG      350
GATTAAAGTT ATCGACTTGC TAGCCCCCTTA CCTTAAGGGT GGTAAGTCG      400
GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG      450
ATTCAACAAC TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT      500
TGGTGAACGT ACACGTGAAG GTAATGACCT TTAAGGGAA ATGAAAGAAT      550
CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA      600
CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA      650
CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT      700
TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG      750
CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT              843

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2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

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TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT      50
AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAGT      100
TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA      150
CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCAGTC      200
GGTAAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA      250
CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA      300
AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA      350
GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT      400

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TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT 450
 TGATTACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA 500
 GTTGCGGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
 ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
 5 CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
 TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
 CTTCCGTTTC ACACAGGCTG GTTCAGAAGT GTCTGCCCTC TTGGGTCGTA 750
 TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
 10 TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTCTGTTA C 841

2) INFORMATION FOR SEQ ID NO: 389

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus uberis*
 25 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
 30 AGGTAGCGAT AAAAACAACAA AGATTGTTCT TGAAGTTGCT TTGGAAGTTG 100
 GGGACGGAAT GGTTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
 CGTGGAATTAG AAGTTTTAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
 AAAAGAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
 TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
 35 GCCCCAGCAT TTGATGAACT ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
 AATAAAAGTT ATTGACTTAT TAGCCCCTTA TCTCAAAGGT GGTAAAGTTG 400
 GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTTAAT TCAAGAATTA 450
 ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTCAAGTAT TTACCGGTGT 500
 TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
 40 CTGGCGTTAT TGAAAAAACA GCCATGGTAT TTGGACAAAT GAACGAACCA 600
 CCAGGAGCAC GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
 TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
 TCCGTTTCAC GCAAGCTGGT TCAGAAGTTT CAGCCCTATT GGGTCGTATG 750
 CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
 45 GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

2) INFORMATION FOR SEQ ID NO: 390

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

5	TTCCCTCAGG	ACGCTGTACC	ACAGGTGTAC	AACGCTCTTG	AGGTTGAAAA	50
	TGGTGATACC	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
	TCGTTCGTAC	GATTGCAATG	GGAACCTCTG	ACGGCCTGAA	ACGTGGCCTT	150
	AAGGTGACCG	ATCTGCAAAA	ACCGATTTCAG	GTACCGGTCG	GTAAAGCGAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGTCA	GCCAATCGAT	ATGAAAGGCG	250
10	ACCTGAAGAA	CGAAGATGGT	AGCAATGTTG	AGGTGAACTC	TATTCACCGT	300
	GCAGCGCCAA	GCTACGAAGA	ACTGGCTAAC	TCTACTGAGC	TGCTGGAAAC	350
	GGGTATCAAG	GTTATCGACC	TGATCTGTCC	GTTTGCAAAA	GGCGGTAAAG	400
	TGGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	AGACCGTCAA	CATGATGGAA	450
	CTGATCCGTA	ACATCGCTAT	CGAGCACTCT	GGTTACTCTG	TATTTGCAGG	500
15	GGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGACCG	550
	AGTCTAACGT	TCTGGATAAA	GTTGCTCTGG	TTTATGGCCA	GATGAACGAG	600
	CCACCAGGAA	ACCGTCTGCG	CGTTGCGCTG	ACCGGTCTGA	CTATGGCTGA	650
	AAAATTCCGT	GACGAAGGCC	GTGACGTACT	GCTGTTTCGT	GATAACATCT	700
	ATCGTTATAC	CCTGGCCGGT	ACTGAAGTTT	CAGCACTGCT	GGGTCGTATG	750
20	CCTTCTGCGG	TAGGTTATCA	GCCAAACTG	GCCGAAGAAA	TGGGTGTTCT	800
	TCAGGAACGT	ATCACGTCAA	CCAAAACCGG	TTCAATCACT	TCCGTA	896

25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trabulsiella guamensis</i>
	(B)	STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

40	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTTATGAA	50
	TGGTAGTGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGTGGTGGTA	100
	TCGTACGTAC	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ATCTCGAGCA	TCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
45	GCTGGGTCGT	ATCATGAACG	TGCTGGGTCA	GCCGATCGAT	ATGAAAGGCG	250
	ACATCGGCCGA	AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCGTCCTAC	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	TCGTAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTGG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCAGAAAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTATC	CCTGGTGTAT	GGACAGATGA	ACGAGCCGCC	GGGAATCCGT	600
	CTGCGCGTTG	CACTGACCGG	TCTGACCATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TACACCCTGG	700
55	CGGGTACTGA	AGTATCTGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CCCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	800
	CTCAACCAAA	ACCGGTTCTA	TCACCTCCG			829

60.

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

CGAATTCCCC	CAAGACGCTG	TACCAAAAGT	GTACAACGCC	CTTGAGGTTG	50
AAGGCACAGC	TCAGAAGCTG	GTGCTGGAAG	TTCAGCAACA	GCTGGGCGGT	100
GGTGTGTGTC	GTTGTATCGC	AATGGGCTCT	TCCGATGGTC	TGAGCCGCGG	150
GTTGAAAGTC	ATCAACCTGG	AACACCCAAT	TGAAGTGCCG	GTGGGTAAAT	200
CAACTCTGGG	CCGTATCATG	AACGTATTGG	GTGACCCAAT	CGACATGAAA	250
GGTCCTATCG	GTGAAGAAGA	GCGTTGGGCA	ATCCACCGCG	AAGCGCCTTC	300
TTACGAAGAG	CTTGCCAGCT	CGCAAGATCT	GTTAGAAACC	GGTATCAAGG	350
TAATGGATCT	GATTTGTCCG	TTCGCTAAGG	GCGGTAAAGT	CGGTCTGTTC	400
GGTGGTGCGG	GTGTGGGTAA	AACAGTCAAC	ATGATGGAGC	TGATTTCGTAA	450
TATTGCGATT	GAGCACTCAG	GTTATTCTGT	ATTTGCCGGT	GTGGGTGAGC	500
GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AGATGACTGA	CTCCAACGTT	550
CTGGACAAAG	TATCCTTGGT	TTATGGCCAG	ATGAATGAGC	CACCAGGTAA	600
CCGTCTGCGC	GTTGCACTGA	CCGGCTTGAC	CATGGCGGAG	AAATTCCGTG	650
ATGAAGGTCTG	TGATGTACTG	TTATTCATCG	ATAACATCTA	TCGTTATAACC	700
CTGGCCCGTA	CAGAGGTATC	TGCACTGCTA	GGTCGTATGC	CATCAGCGGT	750
AGGCTATCAG	CCAACGCTGG	CAGAAGAGAT	GGGTGTGTTG	CAGGAACGTA	800
TCACTTCCAC	CAAGACGGGT	TCAATCACCT	CCGTA		835

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

GCTGTACCAA	AAGTGACAA	CGCCCTTGAG	GTTGAAGGCG	CAGCTGAGAA	50
GCTGGTGCTG	GAAGTTCAGC	AACAGCTGGG	CGGTGGTGTT	GTTTCGTTGTA	100
TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTTGAA	AGTCATCAAC	150
CTGGAACACC	CAATTGAAGT	GCCTGTGGGC	AAGTCAACTC	TGGGCCGTAT	200
CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGCGAAG	250
AAGAGCGTTG	GGCAATCCAT	CGTGAAGCGC	CTTCTTACGA	AGATCTTGCC	300
AGCTCGCAAG	ACTTGTTAGA	AACCGGTATC	AAGGTAATGG	ACTTGATTTG	350
TCCGTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400

	GTAAAACGGT	AAACATGATG	GAGCTTATTC	GTAACATTGC	GATTGAGCAC	450
	TCAGGTTATT	CCGTATTTGC	TGGCGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTTTATGG	CCAAATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
5	CTGACCGGCT	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ATTGCTGTTC	ATCGATAACA	TCTATCGCTA	TACCTTAGCC	GGTACGGAAG	700
	TTTCCGCACT	GCTGGGTCGT	ATGCCATCTG	CCGTAGGTTA	CCAGCCAACG	750
	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACCAAGAC	800
	GGGTTCAATC	AC				812

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2) INFORMATION FOR SEQ ID NO: 394

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
- (B) STRAIN: ATCC 33641

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

	AAAGTGTACA	ACGCCCTTGA	GGTTGAAGGT	ACTGCTGAGA	AGTTAGTACT	50
30	GGAAGTTCAG	CAACAGCTGG	GCGGTGGTGT	TGCTCGTTGT	ATCGCCATGG	100
	GCTCTTCCGA	TGGTTTGAGC	CGCGGGTTGA	AAGTTGTCAA	CCTGGAACAC	150
	CCAATTGAAG	TACCGGTTGG	TAAATCAACT	CTGGGCCGTA	TCATGAACGT	200
	ATTGGGTGAC	CCAATCGACA	TGAAAGGTCC	TATCGGTGAA	GAAGAGCGTT	250
	GGGCAATCCA	CCGCGAAGCG	CCTTCTTACG	AAGAGCTTGC	CAGCTCGCAA	300
35	GATCTGTTAG	AAACCGGTAT	CAAGGTAATG	GATCTGATTT	GCCCGTTCGC	350
	TAAAGGCGGT	AAAGTCGGTC	TGTTCCGTGG	TGCGGGTGTA	GGTAAAACGG	400
	TAAACATGAT	GGAGCTGATC	CGTAATATCG	CGATCGAGCA	CTCAGGTTAT	450
	TCCGTATTTG	CGGGTGTTGG	TGAACGTACC	CGTGAGGGTA	ACGACTTCTA	500
	CCACGAGATG	ACTGACTCCA	ACGTTCTGGA	CAAAGTATCC	TTGGTTTATG	550
40	GCCAGATGAA	TGAGCCACCA	GGTAACCGTC	TTCGCGTTGC	ACTGACCGGT	600
	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	GGTCGTGACG	TATTGCTGTT	650
	CATCGATAAC	ATCTATCGTT	ATACCTTGGC	CGGTACGGAA	GTATCCGCAC	700
	TGCTGGGTCG	TATGCCATCT	GCGGTAGGCT	ATCAGCCAAC	GCTGGCAGAA	750
	GAGATGGGTG	TGTTGCAGGA	ACGTATTACT	TCCACCAAGA	CGGGTTCAAT	800
45	CA					802

2) INFORMATION FOR SEQ ID NO: 395

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*

60

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

5	GCTGTACCAA	GAGTGTACAA	CGCCCTTGAG	GTTGAAGGCA	CTGCTGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AACAGCTAGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GCGGGTTGAA	AGTCATCAAC	150
	CTGGAACACC	CAATTGAAGT	GCCGGTTGGT	AAATCAACTC	TGGGCCGTAT	200
	CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
10	AAGAGCGTTG	GGCAATCCAC	CGCGAAGCGC	CTTCTTACGA	AGAGCTTGCC	300
	AGCTCACAAG	ATTTGTTAGA	AACCGGTATC	AAAGTAATGG	ACTTGATTTG	350
	CCCGTTTCGCT	AAGGGCGGTA	AAGTGGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTA AACAGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTATT	CTGTATTTGC	TGGTGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTGTATGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGTTGTTT	ATCGATAACA	TCTATCGCTA	TACCTTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACG	750
20	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACGT	CCACCAAGAC	800
	GGGTTC					806

25 2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 806 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Yersinia pseudotuberculosis</i>
	(B)	STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

40	GCTGTACCAA	AAGTGTACAA	CGCCCTTGAG	GTAGAAGGCA	CAACTGAAAA	50
	GTTAGTGCTG	GAAGTTCAGC	AACAGTTGGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTTGAA	AGTAACCAAC	150
	CTGGAACACC	CGATCGAAGT	ACCGGTTGGT	AAAGCGACCC	TTGGCCGTAT	200
45	CATGAACGTA	TTGGGTGAAC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCAATCCAT	CGCGAAGCGC	CTTCTTATGA	AGAGCTTGCT	300
	AGCTCACAAG	ATCTGTTAGA	AACCGGTATC	AAGGTTATGG	ACCTGATTTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTA AACAGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
50	TCTGGGTATT	CTGTATTTGC	CGGTGTAGGT	GAGCGTACCC	GTGAGGGTAA	500
	TGACTTCTAC	CATGAAATGA	CTGACTCCAA	CGTTTTGGAC	AAAGTATCCT	550
	TGGTTTACGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	ACGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGCTGTTC	ATCGATAATA	TCTATCGTTA	TACCCTAGCT	GGTACGGAAG	700
55	TATCCGCATT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	TCAGCCAACA	750
	CTGGCTGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACTAAGAC	800
	GGGTTC					806

60

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

TTCCCCCAAG	ACGCTGTACC	AAAAGTGTAC	AACGCCCTTG	AGGTTGAAGG	50
TGCAGCTGAG	AAGCTTGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
TTGTTTCGTTG	TATCGCAATG	GGCTCTTCCG	ATGGTTTGAG	CCGTGGGTTG	150
20 AAAGTTATCA	ACCTGGAACA	CCCAATTGAA	GTGCCAGTTG	GTAAATCAAC	200
TCTGGGCCGT	ATCATGAACG	TATTGGGTGA	CCCAATCGAC	ATGAAAGGCC	250
CTATCGGTGA	AGAAGAGCGT	TGGGCAATCC	ACCGTGAAGC	GCCTTCTTAC	300
GAAGAGCTTG	CCAGCTCGCA	AGATCTGTTA	GAAACCGGTA	TCAAGGTAAT	350
GGATCTGATT	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
25 GTGCGGGTGT	TGGTAAACA	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
GCGATTGAGC	ACTCAGGTTA	TTCTGTATTT	GCCGGGGTAG	GTGAACGTAC	500
TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GA CTGACTCC	AACGTTCTGG	550
ACAAAGTATC	CTTGTTTAT	GGCCAGATGA	ATGAGCCACC	AGGTAACCGT	600
CTGCGCGTTG	CACTGACCGG	CTTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
30 AGGCCGTGAC	GTATTGCTGT	TCATCGATAA	CATTTATCGT	TATACCCTAG	700
CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGC	750
TATCAGCCAA	CACTGGCAGA	AGAGATGGGT	GTGTTGCAGG	AACGTATTAC	800
TTCCACTAAG	ACGGGTTCAA	TCACCTCCG			829

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAAAA	TGGTAACGAG	50
AAACTGGTGC	TGGAAGCTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
55 TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	CCTGGGCCGT	200
ATCATGAACG	TCCTGGGTCA	GCCGATCGAC	ATGAAAGGCG	ACATCGGTGA	250
AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCTTCCTAT	GAAGAGCTGT	300
CCAGCTCTCA	GGAAGTGTG	GAAACCGGTA	TCAAAGTAAT	GGATCTGATC	350
60 TGCCCGTTTCG	CTAAGGGTGG	TAAAGTCGGT	CTGTTTCGGTG	GTGCGGGTGT	400

	AGGTAAAACT	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	GCGATTGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
5	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAAA	800
	ACCGGTTCTA	TCACCTCCG				819

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2) INFORMATION FOR SEQ ID NO: 399

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1097 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Yarrowia lipolytica*

(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
30	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTAATTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTGTTG	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
35	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCTCC	550
40	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGCTCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
45	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
50	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTGCGCC	TCCGAGA	1097

2) INFORMATION FOR SEQ ID NO: 400

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1233 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

10	CAAGCTTAAG	GCTGAACGTG	AGCGTGGTAT	CACCATCGAT	ATCGCTCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACCACGTTA	CCGTCATTGA	TGCCCCCTGGC	100
	CATCGTGATT	TCATCAAGAA	CATGATTACT	GGTACTTCCC	AAGCTGACTG	150
	CGGTATCTTG	ATTATTGCTG	CTGGTACTGG	TGAATTGCGA	GCTGGTATCT	200
	CCAAGGATGG	TCAAACCCGT	GAACACGCTT	TGCTTGCTTT	CACCCTTGGT	250
15	GTCCGTCAT	TGATTGTCGC	TATCAACAAG	ATGGATTCCA	CCAAGTACTC	300
	TGAGGCCCGT	TACAACGAAA	TTGTCAAGGA	AGTCTCCACC	TTCATCAAGA	350
	AGATTGGTTT	CAACCCCAAG	TCCGTTCCCT	TCGTCCCTAT	CTCTGGCTGG	400
	AACGGTGACA	ACATGTTGGA	GGARTCCACC	AACATGCCTT	GGTTCAAGGG	450
	ATGGAACAAG	GAGACTAAGG	CTGGTGCCAA	GACYGGCAAG	ACCCTTCTTG	500
20	AAGCCATTGA	CAACATTGAT	CCCCCTGTTC	GTCCTTCCGA	CAAGCCCCTT	550
	CGTCTTCCCC	TTCAAGATGT	CTACAAGATC	GGTGGTATTG	GTACAGTTCC	600
	TGTCGGTCGT	GTTGAGACTG	TGTGCATCAA	GCCTGGTATG	GTTGTACCTT	650
	TCGCTCCCCG	TAACGTCACC	ACTGAAGTCA	AGTCCGTYGA	AATGCACCAC	700
	GAGCAACTTG	CTGAAGGTGT	TCCCGGTGAC	AACGTCGGTT	TCAACGTCAA	750
25	GAACGTTTCC	GTCAAGGATA	TCCGCCGTGG	TAACGTYTGC	TCTGACTCCA	800
	AGAACGACCC	CGCCAAGGAA	TCCGCTTCCT	TCACCGCTCA	AGTTATTGTC	850
	TTGAACCACC	CTGGTCARAT	TGGTGCTGGT	TACTCTCCTG	TCTTGGATTG	900
	CCCACTGCT	CACATTGCAT	GCAAGTTCTY	TKAGCTTCTT	KAGAAGATCG	950
	ATYGTGCTTC	CGGTAAGTAA	ATANTTTGGT	TTRGGATATG	GGTATTGGGC	1000
30	TTAATCTYTG	GATTTTGCCT	CAATTGCTCC	TTCCTTGATC	TTTCTCGATT	1050
	ACTTTTGTAT	CATTTGCTAA	TCCAAACCCT	TTCCATTTYA	TTGAAAACAG	1100
	GTAAGAAGTT	GGAAGACTCC	CCCAAGTTCG	TCAAGWSYGG	TGACTCTGCY	1150
	ATCGTCAAGA	TGGTTCCTTC	CAAGCCCATG	TGCGTTGAAG	CCTACACTGA	1200
	ATATCCTCCT	CTTGGTCGTT	TCGCTGTCCG	TGA		1233

2) INFORMATION FOR SEQ ID NO: 401

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*
(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

55	CAAGTTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCTCTCT	50
	GGAAGTTCGA	GACTCCCAAG	GTTAGTACCC	CTCTGCCTAC	TACATCAAGT	100
	TCTTTACAAT	GCTAACATGT	TGTACTCAGT	ACTATGTCAC	CGTCATTGAC	150
	GCCCCCGGTC	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	200
	GGCCGACTGC	GCTATTCTCA	TCATTGCCGC	CGGTACTGGT	GAGTTCGAGG	250
	CTGGTATCTC	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	CCTCGCTTAC	300
60	ACCCTCGGTG	TCAAGCAGCT	CATCGTTGCC	ATCAACAAGA	TGGACACCAC	350

	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAAC T'	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCCA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

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2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACTTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCCG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCGTCGGT	CGTGTCGAGA	CTGGTGTCAT	CAAGCCTGGT	700
	ATGGTTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACGAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCCCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
 TTTTTCGCTG CAAGTTCTCT ATAGCTAACA TGA 1283

5

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1103 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: DAL95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
 GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
 ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
 25 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
 CCTCATCATT GCCTCCGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
 ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
 CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
 TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
 30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCACGGT 450
 GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA 500
 GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
 TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
 CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG 650
 35 CCGTGTCGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700
 CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
 CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTC AACG TCAAGAACGT 800
 TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
 ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
 40 CACCCCGGTC AGGTGCGCGC TGGTTACGCC CCCGTCTCG ACTGCCACAC 950
 TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
 GTACCGGCAA GTCTGTTGAG AACAACCCA AGTTCATCAA GTCCGGTGAT 1050
 GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
 CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
5	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCTGGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCTGTC	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACATC	ACCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

30 2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1151 bases
	(B)	TYPE: Nucleic acid
35	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Aspergillus niger</i>
(B)	STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCAATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAACCTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCT	AGACCGGTAT	CATTGCCCCT	GGTATGGTCTG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800
	CGTCAAGAAC	GTTTCCGTCA	AGGAGGTTTCG	CCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCT	CTTGGCTGTG	AGAGCTTCAC	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCCGG	TCAGGTCGGC	GCTGGTTACG	CTCCCGTCCT	950
5	GGACTGCCAC	ACTGCTCACA	TTGCTTGCAA	GTTTCGCTGAG	CTCCTTGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AATCTTCCCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	ATTCCCTCCA	AGCCCATGTG	1100
	TGTTGAGGCT	TTCCTGACT	ACCCCCCTCT	TGGTCGTTTC	GCCGTCCGCG	1150
	A					1151

2) INFORMATION FOR SEQ ID NO: 406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
- (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

	GCTTAAAGCT	GAACGTGAAC	GTGGTATCAC	CATTGATATC	GCTCTCTGGA	50
30	AGTTCGAAAC	TCCTAAGTAC	TACGTTACTG	TTATTGATGC	TCCAGGTCAC	100
	CGTGATTTCA	TCAAGAACAT	GATTACTGGT	ACTTCCCAAG	CCGATTGCGC	150
	CATTCTTATC	ATTGCTGCCG	GTGTCGGTGA	ATTCTGAAGCT	GGTATCTCCA	200
	AGGAAGGTCA	AACCAGAGAA	CACGCTCTTC	TCGCTTTCAC	CCTTGGTGTC	250
	AGACAACCTTA	TCATTGCCAT	CAACAAGATG	GACTCTGTCA	AGTGGGACCA	300
35	AAAGAGATAC	GAAGAAATCG	TCAAGGAGGC	TTCCAACTTC	GTCAAGAAGG	350
	TTGGTTACAA	CCCCAAGTCT	GTTCCATTTCG	TTCTATCTC	TGGTTGGAAC	400
	GGTGACAACA	TGTTGGAACC	TACCACCAAC	GCCCCATGGT	ACAAGGGATG	450
	GACCAAGGAA	ACCAAGGCTG	GTGCCACTAA	GGGTATGACT	CTTATTGAAG	500
	CCATTGACGC	CATTGAACCA	CCAGTAAGAC	CATCCGACAA	GCCACTCCGT	550
40	CTCCCCTCC	AAGATGTTTA	CAAGATTGGT	GGTATCGGAA	CTGTGCCAGT	600
	CGGCCGTGTC	GAAACCGGTA	TCATCAAGGC	CGGTATGGTC	GTTACCTTTG	650
	CTCCACCAAT	GGTCACAAC	GAAGTTAAGT	CCGTGAAAT	GCACCACGAA	700
	CAACTTGCTC	AAGGTAACCC	AGGTGACAAC	GTTGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTT	AAGGAAATCA	GACGTGGTAA	CGTCTGTGGT	GACTCCAAGA	800
45	ACGATCCACC	AAAGGGCTGC	GAATCTTTCA	ACGCTCAAGT	TATCGTCTTG	850
	AACCACCTTG	GTCAAATCTC	TGCTGGTTAC	TCTCCAGTTC	TCGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	GATTTCGACGA	ACTCCTTGAA	AAGATCGACC	950
	GTCGTTCTGG	TAAGAAGATT	GAAGACTCTC	CAAAGTTTGT	CAAGTCTGGT	1000
	GATGCCGCTA	TCGTCAAGAT	GATCCCAACC	AAGCCAATGT	GCGTTGAAAC	1050
50	CTTCACTGAA	TACCCACCAC	TTGGTCGTTT	CGCCGTCCGT	GAT	1093

2) INFORMATION FOR SEQ ID NO: 407

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 10231

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 407

10	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
15	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTYGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
20	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AACTGGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTCGC	CCCAGCTGGT	GTTACCACATG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
25	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCCA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
30	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	A					1101

35 2) INFORMATION FOR SEQ ID NO: 408

(i)SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

- 45 (vi)ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

50 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 408

	GAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	TGATATCGCT	TTGTGGAAAT	50
	TCGAAACTCC	AAAATACCAC	GTTACCGTCA	TTGATGCTCC	AGGTCACAGA	100
	GATTTTCATCA	AGAATATGAT	CACTGGTACT	TCTCAAGCTG	ATTGTGCTAT	150
55	TTTGATTATT	GCTGGTGGTA	CTGGTGAATT	CGAAGCCGGT	ATTTCTAAGG	200
	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACTTT	GGGTGTCAAA	250
	CAATTGATTG	TTGCTGTCAA	CAAGATGGAC	TCTGTCAAAT	GGGACAAAAA	300
	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	CAACTTCGTC	AAGAAGGTTG	350
	GTTACAACCC	AAAGACTGTT	CCATTTCGTT	CAATCTCTGG	TTGGAATGGT	400
60	GACAACATGA	TTGAACCATC	CACCAACTGT	CCATGGTACA	AGGGTTGGGA	450

	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTTGTGAC	TCTTTCAATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTTCG	TGTCAGAGA		1089

15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCA	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTTCTAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
50	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCACCA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAAGTGGT	AAGAAATTCG	AAGAAATTCG	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTC	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

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2) INFORMATION FOR SEQ ID NO: 410

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

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15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAAATTGAT TGTGCTGTC AACAAAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTG  AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
    TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT      400
    GGTGGAATG  GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAATCCGG  TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
    TTAATTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCGGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTGTG  ACTCTTTCAA TGCCCAAGTC      850
    ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCCACA TTGCTTGTA  ATTGACACT TTGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC     1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
    TGTTGAAGCT TTAATGACT  ACCCACCATT AGGTAGATT  GCTGTCAGAG     1100
    AT
  
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2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

```

    CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
60  TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
  
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	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

2) INFORMATION FOR SEQ ID NO: 412

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1101 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - (B) STRAIN: NCPF 3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

5 2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
 (B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
 TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
 GGTACACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
 CTGTGCTATC TTGATCATTG CTTCCGGTGT CCGTGAGTTC GAGGCTGGTA 200
 25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTTGGC CTACACCTTG 250
 GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
 GGACAAGAAC AGATTTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
 AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
 TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
 30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
 TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
 TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
 GCCCGTCGGC CGTGTGCGAGA CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650
 CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
 35 CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTC AACGT 750
 CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAACGTC TCGGGT GACT 800
 CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTTATC 850
 GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900
 CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
 40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
 TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
 TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

45

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTCG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAAGTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCATGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

2) INFORMATION FOR SEQ ID NO: 415

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1102 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

40 (B) STRAIN: CBS 7987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
45	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTYG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850

	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
5	TGTTGAAGCT	TTCCTGACT	ACCCACCATT	AGGTAGATTG	GCTGTCAGAG	1100
	AT					1102

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1094 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Candida famata</i>
(B)	STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25	AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
	AAATTCGAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
	CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
	CTATTTTTRAT	TATTGCTGGT	GGTGTCTGGT	AATTCGAAGC	CGGTATCTCT	200
30	AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
	TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
	AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
	GTTGGTTACA	ACCCTAAGAC	TGTTCCTTTC	GTYCCAATTT	CTGGATGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
35	GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
	GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
	ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
	TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTCACTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
40	ACAATTAGCT	GAAGGTGTTC	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
	AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
	GAACCACCCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
	ACACCGCCCA	CATTGCTTGT	AAATTCGATG	CTTTACTCGA	AAAGATTGAC	950
45	AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTTC	TCAAGTCCGG	1000
	TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
	CTTTCACTGA	ATACCCACCA	TTAGGTAGAT	TCGCTGTTAG	AGAT	1094

50 2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1101 bases
55	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

	TTTGGACAAG	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATCGATATCG	50
	CTTTGTGGAA	GTTCGAAACT	CCAAAGTACC	ACGTYACCGT	TATCGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
10	TGACTGTGCT	ATCTTGATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCYG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTCTATT	GGCTTTTACC	250
	CTAGGTGTTA	GACAATTGAT	TGTYGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	GTGGGATGAA	TCCAGATTCG	CTGAAATCGT	TAAGGAAACC	TCCAACCTCA	350
	TCAAGAAGGT	CGGTTACAAC	CCAAAGACTG	TTCCATTTCG	CCCAATCTCT	400
15	GGTTGGAACG	GTGACAACAT	GATTGAAGCC	ACCACCAACG	CTTCCTGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAGGCTGG	TGTCGTCAAG	GGTAAGACCT	500
	TGTTGGAAGC	CATTGACGCT	ATCGAACCAC	CAACCAGACC	AACTGACAAG	550
	CCATTGAGAT	TGCCATTGCA	AGATGTCTAC	AAGATCGGTG	GTATCGGTAC	600
	GGTGCCAGTC	GGTAGAGTCG	AAACCGGTGT	CATCAAGCCA	GGTATGGTTG	650
20	TTACCTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCACGAAC	AATTGACTGA	AGGTTTGCCA	GGTGACAACG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AGGAAATCAG	AAGAGGTAAT	GTCTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	AAGGCTGCTG	CTTCTTTCAA	CGCTACCGTC	850
	ATTGTCTTGA	ACCACCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTTTT	900
25	GGACTGTCAC	ACCGCCACAC	TTGCTTGTA	GTTCGAAGAA	TTGTTGGAAA	950
	AGAACGACAG	AAGATCCGGT	AAGAAGTTGG	AAGACTCTCC	AAAGTTCTTG	1000
	AAGTCCGGTG	ACGCTGCTTT	GGTTAAGTTC	GTTCCATCCA	AGCCAATGTG	1050
	TGTCGAAGCT	TTCTCCGACT	ACCCACCATT	GGGTAGATTC	GCTGTCAGAG	1100
	A					1101

30

2) INFORMATION FOR SEQ ID NO: 418

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

	AGAGAAAGAG	GTATCACCAT	TGACATTGCT	TTGTGGAAAT	TCGAGACTCC	50
50	AAAGTACCAC	GTTACYGTCA	TTGATGCCCC	AGGTACACAG	GATTTTCATCA	100
	AGAACATGAT	CACTGGTACT	TCTCAAGCTG	ACTGTGCTAT	TTTGATTATT	150
	GCTGGTGGTA	CCTGGTGAAT	CGAAGCTGGT	ATCTCTAAGG	ATGGTCAAAC	200
	CAGAGAGCAC	GCTTTGTTGG	CTTACACCTT	GGGTGTTAGA	CAATTGATTG	250
	TTGCTGTCAA	CAAGATGGAC	TCCGTCAART	GGGACAAGAA	CAGATTYGAG	300
55	GAAATCATCA	AGGAAACCTC	TAACCTCGTC	AAGAAGGTTG	GTTACAACCC	350
	TAAGACTGTG	CCATTCGTTT	CTATCTCTGG	ATGGAAYGGT	GACAACATGA	400
	TTGAGGCTTC	TACCAACTGT	CCTTGGTACA	AGGGATGGGA	GAAGGAGACC	450
	AAGGCTGGTA	AGTCCACCGG	TAAGACTTTG	TTGGAGGCCA	TTGACGCCAT	500
	TGAGCCACCT	CAAAGACCAA	CCGACAAGCC	ATTGAGATTG	CCATTGCAAG	550
60	ATGTYTACAA	GATTGGTGGT	ATTGGAACGG	TGCCAGTCGG	TAGAGTTGAA	600

	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	ACTGTCACAC	CGCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTGG	GAAGATTTCG	CGTCAGAGAC			1080

2) INFORMATION FOR SEQ ID NO: 419

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAAGTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGTGGTGTT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
	CCAGTTTTTG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

2) INFORMATION FOR SEQ ID NO: 420

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*

60

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

5	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAGTATC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	TAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
	AGATTGTGCT	ATTTTGTATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GSTATTTCCAA	GGATGGTCAA	ACTAGAGAAC	ACGCTTTATT	AGCATTTCACC	250
10	TTAGGTGTTA	AGCAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCTGTATA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTTCTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTCAAG	GGTAAGACCT	500
15	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGATAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTAT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAAGA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
20	CGTCAAGAAC	GTCTCTGTTA	AGGATATCAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	TGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCTGG	TCAAATTTCT	GCTGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCACAC	TTGCATGTAA	ATTTCGATGAA	TTAATTGAAA	950
	AGATTGACAG	AAGAAGTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
25	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	AT					1102

30

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1099 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Candida kefyr</i>
(B)	STRAIN: ATCC 28838

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

	TGGACAAGTT	AAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	CGATATCGCT	50
	TTGTGGAAGT	TCGAAACTCC	AAAGTACCAA	GTTACCGTTA	TCGATGCTCC	100
	AGGTCACAGA	GATTTTCATCA	AGAACATGAT	TACTGGTACT	TCTCAAGCTG	150
50	ACTGTGCTAT	CTTGATTATT	GCTGGTGGTG	TCGGTGAATT	CGAAGCCGGT	200
	ATCTCCAAGG	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACCTT	250
	GGGTGTTAGA	CAATTGATTG	TTGCTATCAA	CAAGATGGAC	TCTGTTAAGT	300
	GGGATGAATC	TCGTTACCAA	GAAATTGTTA	AGGAAACCTC	CAACTTCATC	350
	AAGAAGGTCC	GTTACAACCC	AAAGAATGTT	CCATTTCGTCC	CAATCTCTGG	400
55	TTGGAACGGT	GACAACATGA	TTGAAGCCAC	CACCAACGCT	CCATGGTACA	450
	AGGGTTGGGA	AAAGGAAACC	AAGGCTGGTA	CCGTCAAGGG	TAAGACCTTG	500
	TTGGAAGCTA	TTGACGCTAT	CGAACCACCA	ACCAGACCAA	CTGACAAGCC	550
	ATTGAGATTG	CCATTGCAAG	ATGTCTACAA	GATCGGTGGT	ATTGGTACTG	600
	TGCCAGTCGG	TAGAGTCGAA	ACCGGTGTCA	TCAAGCCAGG	TATGGTTGTT	650
60	ACCTTCGCCC	CAGCCGGTGT	CACTACCGAA	GTTAAGTCCG	TCGAAATGCA	700

CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	900
ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
GTCTGGTGAC	GCTGCTTTGG	TTAAGTTTCGT	TCCATCTAAG	CCAATGTGTG	1050
TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
 (B) STRAIN: ATCC 34135

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
GCTATTTTGA	TTATTGCTGG	TGGTGTCGGT	GAATTCGAAG	CTGGTATCTC	200
CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
GTCGGTAGAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCACTTT	650
TGCTCCAGCA	GGTGTACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
GCTTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 5 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

	CTTGGACAAG	CTTAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
10	CTTTATGGAA	GTTTCGAACT	CCAAAGTACC	ACGTTACCGT	CATTGACGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATTACTGGTA	CCTCTCAAGC	150
	AGATTGTGCT	ATTTTTRATYA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTCTTCT	TGCATTCACT	250
	CTTGGTGTTA	GACAATTGAT	TGTTGCTATC	AACAAGATGG	ACTCTGTCAA	300
15	GTGGGACGAA	TCCAGATTCG	ATGAAATTTG	TAAGGAAACC	GCWAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	CCCAATCTCT	400
	GGTTGGAACG	GTGACAACAT	GATTGAACCA	TCTGCTAACT	GTCCATGGTA	450
	CAAGGGATGG	ACTAAGGAAA	CCAAGGCTTC	CGGTGTCGTC	AAGGGTAAGA	500
	CCCTTCTTGA	AGCAATTGAT	GCTATTGAGC	CACCTGTCAG	ACCAACTGAC	550
20	AAGGCTTTGA	GATTGCCATT	RCAAGATGTC	TACAAGATTG	GTGGTATTGG	600
	TACTGTGCCA	GTCGGTAGAG	TTGAAACCGG	TATCATCAAG	CCAGGTATGA	650
	TTGTCGTTTT	CGCTCCAACC	GGTGTTACTA	CTGAAGTTAA	GTCCGTTGAA	700
	ATGCACCATG	AACAATTAGA	AGAAGGTGTC	CCAGGTGACA	ATGTTGGTTT	750
	CAACGTCAAG	AACGTCTCTG	TTAAGGATAT	TAAGAGAGGT	AACGTCTGTG	800
25	GTGACTCCAA	GAACGACCCA	CCAATGGGTT	GTGCTTCCTT	CAATGCTCAA	850
	GTCATTGTTC	TTAACCACCC	AGGTCAAATT	TCTGCTGGTT	ACTCACCAGT	900
	TCTTGACTGT	CACACTGCCC	ACATTGCATG	TAAGTTCGAY	GAATTACTCG	950
	AAAAGATTGA	CAGAAGAACC	GGTAAGGCTA	CTGAAGACCA	TCCAAAGTCT	1000
	GTCAAGTCTG	GTGATGCAGC	TATCGTCAAG	ATGGTTCCAA	CCAAGCCAAT	1050
30	GTGTGTYGAA	GCTTTCACTG	ACTACCCACC	ATTAGGTAGA	TTCGCTGTYA	1100
	GAGA					1104

35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

50	GGACAAGTTG	AAGGCTGAGA	GAGAAAGAGG	TATCACCATC	GATATCGCTT	50
	TGTGGAAGTT	CGAGACTCCA	AAGTACCACG	TTACCGTCAT	TGACGCTCCA	100
	GGTCACAGAG	ATTTTCATCAA	GAACATGATC	ACTGGTACTT	CCCAAGCTGA	150
	CTGTGCTATC	TTGATTATCG	CTGGTGGTGT	CGGTGAGTTC	GAAGCCGGTA	200
55	TCTCTAAGGA	CGGTCAAACC	AGAGAGCACG	CTTTGTTGGC	TTACACCTTG	250
	GGTGTCAAGC	AGTTGATTGT	TGCTGTCAAC	AAGATGGACT	CCGTCAAGTG	300
	GGACCAATCT	AGATTCGAGG	AAATCATCAA	GGAAACCTCT	AACTTCGTCA	350
	AGAAGGTTGG	TTACAACCCT	AAGACTGTTT	CATTCGTCCC	AATCTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGCCATCY	ACCAACTGCC	CATGGTACAA	450
60	GGGTTGGGAG	AAGGAGACCA	AGTCYGGTAA	GTCCACCGGT	AAGACCTTGT	500

	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAAGCCA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTTCAT	CAAGGCCCGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTG	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCAGTGC	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTTCGCT	GTCAGAGA	1098

15

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCACC	250
	TTAGGTGTGA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTG	AAGAAATTGT	CAAGGAAACC	CAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTAAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTGA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTGTGT	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCACA	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
A						1101

55

2) INFORMATION FOR SEQ ID NO: 426

60 (i) SEQUENCE CHARACTERISTICS:

257

(A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

15	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
	GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTAAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCTGA	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCCT	GACTACCCAC	CATTGGGAAG	ATTCGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCTGA	GGAGATCGTC	AAGGAGGTTT	50
	CCAAGTTTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCCTCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
60	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCG	350
	GCATGGTCGT	CAC TTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTCGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTCAA	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTTTG	GACTGCCACA	CCGCCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

2) INFORMATION FOR SEQ ID NO: 428

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTCGGTG	AATTGGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCCGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAACTT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATTCCAGA	CCAACTGACA	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCTGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	AACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

10
 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG 50
 GAAATTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100
 ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT 150
 GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTT 200
 15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG 250
 TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC 300
 AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA 350
 GGTTGGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA 400
 ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT 450
 20 TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTTGGA 500
 AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA 550
 GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600
 GTCGGTAGAG TTGAAACTGG TGTCATCAAA GCCGGTATGG TTGTTACTTT 650
 CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG 700
 25 AACCAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750
 AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA 800
 GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT 850
 TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT 900
 CACACTGCTC ATATTGCTTG TAAATTGAC ACCTTGGTTG AAAAGATTGA 950
 30 CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG 1000
 GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA 1050
 GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA 1094

35

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT 50
 GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT 100
 CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG 150
 55 TGCTATTCTT ATCATTGCCG GTGGTGTGG TGAGTTCGAG GCTGGTATCT 200
 CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT 250
 GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA 300
 CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA 350
 AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG 400
 60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG 450

260

	TTGGGAGAAG	GAGACCAAGG	CTGGTGTGTG	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAACGTGTTCC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1085 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AAC TGCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAACGTGACC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCACT	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

261

(A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

15	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTCGAGACC	CCCAAGTACC	50
	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCTG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTG GTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCC	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCGG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCACA	TTGCTTGCGAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCCTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCTGGTC	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTCATCAA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

2) INFORMATION FOR SEQ ID NO: 434

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTG	50
	GAAGTTCGAG	ACCCCAAGT	ACAATGTCAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCCG	ACAAGCCCTT	600
	GCGATTGCCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTCGGTCG	AGTCGAGACC	GGTGTCATCA	AGGCTGGTAT	GGTCGTCACC	700
	TTCGCCCCTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TTCAACGCTC	AGGTCATTGT	900
	CTTGAACCAC	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTGC	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTCGCCGT	CCGAGA	1146

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

	CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTCATCGA	CGCCCCTGGT	100
	CATCGTGACT	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15	CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTCGAA	GCCGGTATCT	200
	CCAAGGATGG	TCAGACTCGT	GAGCACGCTC	TGCTCGCCTA	CACCCTGGGT	250
	GTCAAGCAGC	TCATTGTGCG	CATCAACAAG	ATGGACACCA	CCAAGTGATC	300
	CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
	AGGTCGGCTA	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	400
20	AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCCC	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
	AGGCCATCGA	CGCCATCGAC	CCCCCACTC	GTCCCACCGA	CAAGCCTCTC	550
	CGTCTTCCTC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
	CGTCGGTTCG	GTTGAGACTG	GTGTCATCAA	GGCCGGTATG	GTCGTTACCT	650
25	TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
	GAACAACCTC	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGAGG	TTCGTCGTGG	AAACGTCTGC	GGTGACTCCA	800
	AGAACGACCC	ACCCAAGGGT	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	850
	TTGAACCACC	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30	CCACACTGCC	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATTG	950
	ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	1000
	GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CTCTTGGTCT	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTCGC	100
55	TCATGCTTCA	TTCTACTTCT	CTTCGTACTA	ACACATCACT	CAGACGCTCC	150
	CGGTCACCGT	GATTTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
	ATTGCGCCAT	TCTCATCATT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCT	300
	TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTCACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTACAC	TGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

2) INFORMATION FOR SEQ ID NO: 437

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAAGGAGAC	AAGGCTGGTG	TCACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAACCTG	300
	TGCCCCGTCGG	CCGTGTCGAA	ACCGGTGTCA	TCAAGGCCGG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCGG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTAAAG	GATATCAGAC	GTGGTAACGT	CTGCGGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTC AACG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCTGGTC	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTA CTGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

50

2) INFORMATION FOR SEQ ID NO: 438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

(B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

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10  CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
    CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
    CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAACTG      150
    CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
    GTAAAACCCT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
    ACCGATAAGC CCCTCCGTCT TCCCTCCAG GATGTGTACA AAATCTCTGG      300
15  TATTGGCACT GTTCCCGTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCCG      350
    GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
    GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT      450
    CGGCTTCAAC GTCAAGAACG TTTCAGTCAA GGAAGTCCGC CGTGGAACG      500
    TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
20  GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
    CCCAGTCCTC GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC      650
    TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
    AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
    GCCC
25

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2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Issatchenkia orientalis*

(B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

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45  TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
    CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTTCGT CCAATCTCTG      100
    GTTGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
    AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
    ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
    CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
50  GTGCCAGTCG GTAGAGTCGA AACC GGTTGTC ATTAAGCCAG GTATGGTTGT      350
    CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
    ACCATGAACA ATTAGAACA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
    GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGTGA      500
    CTCCAAGAAC GACCCACCAA TGGGTGCGAG TTCYTTCAAT GCTCAAGTCA      550
55  TTGTCTTGAA CCACCCTGGT CAAATTTCCG CTGGTTACTC TCCAGTCTTG      600
    GATTGTCACA CTGCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
    GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
    AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC          743

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60

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT 50
 GGAAGTTCGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT 100
 20 CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG 150
 CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT 200
 CGAAGGACGG TCAGACCCGT GAGCAGCTC TGCTCGCTTT CACCCTGGGT 250
 GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC 300
 GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTCGAAC TTCATCAAGA 350
 25 AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCAT CTCGGGCTGG 400
 CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG 450
 CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG 500
 ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCCTGA CAAGCCCCTG 550
 CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC 600
 30 TGTCGGTCGT GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT 650
 TCGTCCCTC GAACGTCACC ACTGAAGTTA AGTCGGTTGA GATGCACCAC 700
 GAGTCGCTCC CTGAGGGTCT CCCCAGGTGAC AACGTTGGTT TCAACGTGAA 750
 GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA 800
 AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCATTGTC 850
 35 ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCC TGCTTGACTG 900
 CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG 950
 ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCAAGTT CATCAAGTCG 1000
 GGTGACGCTG CCATGGTGGG ATGATCCCC ACCAAGCCCA TGTGTGTGGA 1050
 40 GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTCGCTGTG C 1091

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 55 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC 50
 60 GAACTTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC 100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCCGGTCGG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTAAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTTCGCC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRGTTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTTCGACATG	100
35	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCGG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCTGTGTCG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTCGCAG	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCTGGTG	TGGATACGCT	CCCGTCTCTG	950
	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCTTGG	GTCGTTTCGC	CGTCCGTGAC	1150

2) INFORMATION FOR SEQ ID NO: 443

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

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15  GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT      50
    TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA      100
    GGTACACAGAG ATTTTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA      150
    CTGTGTCYATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA      200
    TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTGTTGGC YTACACCTTG      250
20  GGTGTTAGAC ARTTGATTGT TGCCGTCAAC AAGATGGACT CTGTCAAGTG      300
    GGACAAGAAC AGATTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA      350
    AGAAGGTTGG TTACAACCCT AAGACYGTGC CATTTCGTGCC AATYTCTGGT      400
    TGAACCGGTG ACAACATGAT TGAGGCYTCC ACTAACTGCC CATGGTACAA      450
    GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT      500
25  TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC      550
    TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT      600
    GCCAGTCGGC CGTGTGCGAG CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA      650
    CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC      700
    CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCAACGT      750
30  CAAGAACGTC TCCGTTAAGG AGATCAGAAG AGGTAACGTC TGTGGTGACT      800
    CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT      850
    GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTACTCTC CAGTGTGGGA      900
    CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA      950
    TTGACAGAAG AACTGGTAAG TCCTTGAGAGT CYGAGCCTAA GTTCGTCAAG     1000
35  TCYGGTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT     1050
    TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTCGCC GTCAGAGAC     1099
  
```

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

```

55  CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
    GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT      100
    CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG      150
    CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCCAG      200
60  GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCCTGGTG AGTTCGAGGC      250
  
```

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTTCA	300
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350
	AAGTGGTCTG	AGGCCCGTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACCT	400
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	450
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCTGG	500
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	550
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCGAGCGACA	600
	AGCCCCTCCG	CCTTCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	650
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	700
10	CGTGACCTTC	GCTCCTTCCA	ACGTCACCAC	CGAAGTCAAG	TCCGTTGAGA	750
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	ACGTCGCCGG	850
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGGTCG	GTGCTGGCTA	CGCCCCCGTC	950
15	CTCGACTGCC	ACACCGCCCA	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1000
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1050
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1100
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1150
20	TGA					1153

2) INFORMATION FOR SEQ ID NO: 445

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 763 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTCCTGTCT	GACGTGTTGA	GAAGTGGAGT	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
50	CCCCAGGTCA	TCGTCCTCAA	CCACCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCACAT	TGCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACC GGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
55	GGCCATGTGC	GTC				763

2) INFORMATION FOR SEQ ID NO: 446

- (i) SEQUENCE CHARACTERISTICS:

270

(A) LENGTH: 1346 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 64101

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTCCCT	TTCGTTCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCCGGT	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGTACC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACGCCAAG	TTATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60 AAGTTAAAAG CTGAACGTGA AAGAGGTATC ACTATTGATA TTGCTTTATG 50

	GAAATTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCAC	ACTACCCACC	ATTAGGTCGT	TTGCTGTCA	GAGA	1094

25 2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACTTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAAC	TCCATTTCGT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAAC	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA	TGCTGCTATT	GTAAATTTG	TTCCATCAAA	ACCATATCA	1050
GTTGAAGCTT	TCACTGACTA	CCCACCATTA	GGTCGTTTCG	CTGTCAGAGA	1100

5

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1201 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
(B) STRAIN: ATCC 44331

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
GGAAGTTCGA	GACCCCAAG	TACCAGGTCA	CCGTCATTGG	TATGTCCTTG	100
TGCTTTTGT	GCTTTTGTG	CCTGTGCCTC	GCACAATTCC	AGCCCTCGAT	150
25 AATTATGAAC	CTCGTACTAA	TATGTCGTTC	TCCCCTACC	CACAGACGCC	200
CCCGGCCATC	GTGATTTTCA	CAAGAACATG	ATTACTGGTA	CCTCCCAGGC	250
TGATTGCGCC	ATTCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	300
GCATCTCCAA	GGATGGCCAG	ACCCGTGAGC	ACGCTCTTCT	CGCCTTCACC	350
CTCGGTGTCA	AGAACCTCAT	TGTTGCCATC	AACAAGATGG	ACACCAACAA	400
30 CTGGTCCGAG	GACCGATACA	AGGAGATCAT	CAAGGAGACC	TCCAACCTCA	450
TCAAGAAGGT	CGGCTACAAC	CCCAAGGCCG	TTCCTTTTCGT	CCCCATCTCC	500
GGTTTCCACG	GAGACAACAT	GCTTACCCCC	TCCACCAACT	GCCCCTGGTA	550
CAAGGGTTGG	GTCCGTGAGG	TCAAGGGTAA	CACCCTTACC	GGCAAGACCC	600
TTCTCGAGGC	CATCGACTYC	ATCGAGCCCC	CCAAGCGTCC	CACCGAGAAG	650
35 CCCCTCCGTC	TTCCCCTTCA	GGACGTCTAC	AAGATCGGTG	GTATTGGCAC	700
TGTGCCCGTC	GGCCGTATCG	AGACCGGTAT	CCTCAAGCCC	GGTATGGTCG	750
TCACCTTCGC	TCCCTCCAAC	GTCACCATG	AAGTCAAGTC	CGTCGAGATG	800
CACCACGAGC	AGCTTACCGA	GGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	850
CGTGAAGAAC	GTCTCCGTCA	AGGATATCCG	CCGTGGCAAC	GTCTGCGGTG	900
40 ACTCCAAGAA	CGACCCCCCC	GCTGCTGCCG	CCTCTTTCCA	GGCCCAGGTC	950
ATTGTCCTCA	ACCACCCCGG	CCAGATCGGT	GCTGGTTACG	CTCCCGTTCT	1000
TGACTGCCAC	ACTGCCACAA	TTGCTTGCAA	GTTCGCCGAG	CTCCTTGAGA	1050
AGATCGACCG	CCGTACCGGT	AAGTCGGTCG	AGAACAACCC	CAAGTTCGTC	1100
AAGTCTGGTG	ATGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1150
45 TGTTGAGTCC	TTCACCGAGT	ACCCCCCTCT	CGGTCGTTTC	GCCGTCCGTG	1200
A					1201

50 2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*

(B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

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5  CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT 50
   GGAAGTTCTGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT 100
   CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG 150
   TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTGCAA GCTGGTATCT 200
10 CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT 250
   GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC 300
   CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA 350
   AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG 400
   CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG 450
15 ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG 500
   ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC 550
   CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC 600
   CGTCGGTCGT GTCGAAACTG GTGTCATCAA GGCTGGTATG GTTGTACCT 650
   TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC 700
20 GAAACCCTCA CTGAAGGTCT CCCCAGGTGAC AACGTCGGTT TCAACGTCAA 750
   GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA 800
   AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC 850
   TTGAACCACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG 900
   TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG 950
25 ACAGACGTTT CGGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT 1000
   GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA 1050
   AGCTTACACT GACTACCCTC CTCTCGGTCG TTTCGCTGTT CGTGA 1095

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30

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

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35 (A) LENGTH: 1092 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*

(B) STRAIN: ATCC 10658

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

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   GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA 50
   AGTTCGAGAC CCCCAGGTAC AACGTCACCG TCATTGACGC TCCAGGACAT 100
   CGTGATTTCA TCAAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA 150
50 CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTAATTCCCA 200
   GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC 300
   ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT 350
   CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC 400
55 CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC 450
   GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCTG ACCCCAAGGG 500
   TGTTCCCTTC GTCCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG 550
   AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC 600
   GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC 650
60 CCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT 700

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	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTTC	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	GGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCCT	CCAGGTTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCTGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTGCTCGGC	900
50	CATTTTTTCA	GTCTTGACCC	CGTTTTGCCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCAA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

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GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA 100
GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
20 CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
CGTGAGCAGC CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
AAGACTGTTG CTTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
25 TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
GAGCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCTGC CGTATCGAGA 600
CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
30 ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA 850
GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
35 CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
CCCCTCTGGG CCGTTTCGCC
1070

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2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

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CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
60 GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150

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	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTCGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGAGAGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCCTCTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
20	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092

2) INFORMATION FOR SEQ ID NO: 455

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
- (B) STRAIN: WSA-225

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTTCT	CTTTACCTTT	100
	CCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAACCTG	650
	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCTGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC CGTCCGTGA' f149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
 CCAGGTCACC GTGATTTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
 25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
 CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300
 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACTTCG 350
 TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTTCGT TCCTATCTCT 400
 GGTGGAACG GTGACAACAT GTTGAACCT ACCACCAACG CCCCATGGTA 450
 30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
 CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
 TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
 TCACCTTTGC TCCACCAATG GTCACAACCTG AAGTTAAGTC CGTTGAAATG 700
 35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
 CGTCAAGAAC GTTTCCGTTA AGGAAATCAG ACGTGGTAAAC GTCTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
 ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900
 CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTGACGAA CTCCTTGAAA 950
 40 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
 AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
 CGTTGAAACC TTCCTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100
 A 1101

45

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

	GTTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TATGTCACCG	TCATCGACGC	CCCGGGTCAT	100
5	CGTGACTTTA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATCTTGATC	ATTGCCGCCG	GTACCGGTGA	ATTCGAAGCC	GGTATCTCCA	200
	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	TCGCCTACAC	CTTGGGTGTC	250
	AAGCAGCTCA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	300
	GGAGCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACTTC	ATCAAGAAGG	350
10	TCGGCTACAA	CCCCAAGGCC	GTTCCTTTTCG	TCCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATTGAGGT	CTCCACCAAC	TGCCCGTGGT	ACAAGGGATG	450
	GGAGAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTCGAGG	500
	CCATTGACGC	CATCGACCCA	CCCACCCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCTCTCC	AGGATGTCTA	CAAGATCTCT	GGTATCGGAA	CGGTTCTGT	600
15	CGGTCTGTGC	GAGACCGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTCG	650
	CTCCGGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAG	700
	CAGCTCGCCG	AGGGTCTGCC	AGGTGACAAC	GTTGGCTTCA	ACGTCAAGAA	750
	CGTCTCCGTC	AAGGAGGTTC	GTCGTGGTAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCGCC	CAAGGGTGCC	GAGTCCTTCA	ACGCCCAGGT	CATTGTCCTC	850
20	AACCACCCTG	GTCAGATCGG	TGCCGGCTAC	GCTCCAGTCT	TGGATTGCCA	900
	CACTGCCAC	ATTGCTTGCA	AGTTCGCCGA	GTTGCTCGAG	AAGATCGACC	950
	GTCGTACCGG	AAAGTCCATC	GAGAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
	GATGCTGCCA	TCGTCAAGAT	GATTCCCAGC	AAGCCCATGT	GTGTCGAGGC	1050
25	TTTCACCGAC	TATCCTCCTC	TGGGTCGTTT	CGCTG		1085

2) INFORMATION FOR SEQ ID NO: 458

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: DAL-95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

	TGTCTTCATC	CGGAATTGAT	TGTGAGTCGT	TCCACATGCT	CACCTAGTTT	50
45	TCGCTCGATC	TTTTCACTAA	CGCAAACCAT	GTAGAACAAAC	ATTGCCAAGG	100
	CCCACGGTGG	TTACTCCGTC	TTCACTGGTG	TTGGTGAGCG	TACTCGTGAG	150
	GGTAACGATC	TGTACCACGA	AATGCAGGAG	ACTGGTGTC	TTCAGCTCGA	200
	GGGTGAATCC	AAGGTCGCAC	TGGTGTTCGG	ACAGATGAAC	GAGCCCCCGG	250
	GTGCCCGTGC	CCGTGTCGCC	CTTACCGGTC	TGACCATTGC	CGAGTACTTC	300
50	CGTGACGAGG	AGGGTCAGGA	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	350
	TTTCAACCCAG	GCCGGTTCTG	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	400
	CTGCCGTCGG	TTACCAGCCC	ACCCTGGCCG	TCGACATGGG	TGGTATGCAG	450
	GAGCGTATCA	CCACCACCAA	GAAGGGTTCT	ATTACCTCCG	TC	492

2) INFORMATION FOR SEQ ID NO: 459

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTGGT	ACTCTTGGTA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAACTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GACTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGTCTCG	800
	TTCCATTTCC	GAATTGGGTA	TCTACCCAGC	TGTCGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAAGATC	CAAAGATTCC	TTTCCCAACC	ATTGCTGTGT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55	CCAATTGCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTACTTTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAACC	GGTATCAAGG	350
	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTGCGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTCATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCATTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTCGATC	CATTGGATTG	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

25 2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAACTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCCG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTG	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTCGCCCCA	900
	TTTGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTT	AAACAACTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTCA	CTGGTATTCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTC	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

10 2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1278 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Candida famata</i>
(B)	STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTT	TGCC	AGCT	ATTTTG	AACG	CTTTGA	CCTT	GAAGAA	CGGT	GAAAAC	50
	GAC	TTAG	TTT	TAGA	AGTTGC	CCA	ACATTTG	GGT	GAAAACA	CCGT	CAGAGC	100
	TATT	GC	TATG	GATG	GTACTG	AAG	TTTAGT	TAG	AGGTACT	CCAG	TTACCG	150
	ATT	CTGG	TGC	TCCA	ATTTCT	GT	CCCAGTCG	GTA	GAGGTAC	TTTA	GGTAGA	200
30	AT	CTTGA	ACG	TTAT	TGGTGA	ACCA	ATTGAT	GA	ACAAGGTC	CAG	TTGATGC	250
	CA	AGGAA	ACC	AGAC	CAATTC	ACCA	AAGACCC	ACC	AGCATTC	GTT	GATCAAT	300
	CC	ACCA	AGGC	TGA	AGTTTTG	GAA	ACTGGTA	TCA	AGGTTGT	CGAT	TTTATTA	350
	GCC	CCTT	ACG	CTAG	AGGTGG	TA	AGATTGGT	TTAT	TCGGTG	GTG	CCGGTGT	400
	CG	GTA	AGACC	GTCT	TTTATCC	AAG	AATTGAT	TA	ACAACATT	GCCA	AGGCCC	450
35	AT	GGTGG	TTT	CTCT	GTTTTT	ACT	GGTGTCG	GT	GAAAGAAC	CAG	AGAAGGT	500
	AAC	GATTT	TAT	ATAG	AGAAAT	GA	AGGAACT	GGT	GTCATTA	ACT	TGGAAGG	550
	TG	ACTCCA	AAG	GTCG	CCTTGG	TTTT	CGGTCA	AAT	GAACGAA	CCAC	CAGGTG	600
	CT	AGAGCT	AG	TTGCT	TTTA	ACCG	GTTTAA	CCAT	TGCCGA	ATA	CTTCAGA	650
	GAC	GAAGA	AAG	GTCA	AGATGT	GTT	ATTGTTT	GTC	GATAACA	TTTT	TTAGATT	700
40	CAC	CCAAG	CC	GGTT	CCGAAG	TGT	CTGCTTT	GTT	AGGTCGT	ATT	CCATCGG	750
	CT	GTCGG	TTA	TCA	ACCAACC	TTAG	CCACTG	ATAT	GGGTCT	TTTA	CAAGAA	800
	AGA	ATTAC	CA	CCAC	CAACAA	GGGT	TCCGTT	ACT	TCTGTCC	AAG	CTGTCTA	850
	CG	TCCAG	CC	GATG	ATTTAA	CCG	ATCCTGC	TCC	AGCTACC	ACT	TTTCGCC	900
	ACT	TGGAT	GC	TAC	CACTGTG	TTGT	CTCGTG	GTAT	CTCTGA	ATT	GGGTATT	950
45	TAC	CCAG	CTG	TCG	ATCCATT	GGAT	TCCAAA	TCC	GATTGT	TAG	ATGCTGA	1000
	TAT	CGTT	GGT	AA	GAACACT	AC	GAAGTTGC	CA	CTGGTGTC	CA	ACAAACCT	1050
	TAC	AAGCT	TA	CAA	ATCTTTA	CA	AGATATCA	TT	GCTATTTT	AG	GATGGAT	1100
	GA	ATTGT	CTG	AAG	CCGATAA	ATT	GACTGTC	GAA	AGAGCCA	GAA	AGATCCA	1150
	AAG	ATTCT	TTG	TCT	CAACCAT	TCG	CCGTTGC	CGA	AGTTTTT	ACC	GGTATCC	1200
50	CAG	GTA	GATT	AG	TTAGATTG	CA	AGACACTG	TTA	AATCTTT	CA	AGGAAGTC	1250
	TT	GAA	AGGTA	AAT	ATGATCA	CTT	ACCAG					1278

55 2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1154 bases
	(B)	TYPE: Nucleic acid
60	(C)	STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

```

10 TCTGGTCAGA GCGGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC      50
   CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT      100
   ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC      150
   CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA      200
15 CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG      250
   ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA      300
   ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTACAG      350
   GTGTCGGTGA AAGAACCAGA GAAGGTACG ATTTGTACAG AGAAATGAAG      400
   GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT      450
20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG      500
   GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG      550
   CTGTTTCGTCG ACAACATTTT CAGATTACC CAAGCCGGTT CAGAAGTCTC      600
   CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG      650
   CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT      700
25 TCCGTCACCT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA      750
   TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCCTGT      800
   CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCGA CCCATTGGAC      850
   TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA      900
   CGTCGCCACA AAGGTCCAAG AAACTTTACA AACTTACAAG TCTCTGCAAG      950
30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA     1000
   ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCT AACCATTCCG     1050
   TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG     1100
   ACACCATCTC CTCTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT     1150
   CCAG                                                                1154

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2) INFORMATION FOR SEQ ID NO: 464

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40 (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 1293 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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45 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Candida guilliermondii*

(B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

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55 CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA      50
   AGAACGGTGA CCAAAACTTG GTTTTGGAAG TTGCCCAGCA TTTGGGTGAA      100
   AACACCGTCA GAACCATTCG TATGGATGGT ACTGAAGGTT TGGTTAGAGG      150
   TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG      200
   GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT      250
   GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTACGCTG AACCACCATC      300
60 GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG      350

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	TTGTCGACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTG	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTACCCGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTCGTCGAC	700
	AACATTTTCA	GATTCACTCA	AGCTGGTTCT	GAAGTGTCGG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTTGCA	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTCGATC	CTTTGGATTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

2) INFORMATION FOR SEQ ID NO: 465

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1293 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Candida haemulonii*
- (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGGAGGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTTCG	400
	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTCG	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAAGG	TGTGTTGTTG	TTCTGTGACA	700
	ACATTTTCAG	ATTCACCTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTTCG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTT	950
	CGAGTTGGGT	ATCTACCCAG	CTGTGACCCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCAC TGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1111 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	TATTAAGGTT	300
GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTTCGG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCACTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACCTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTTCGGT	CAAATGAATG	550
AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	TTACTTCTGT	800
CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
CTACTTTCGC	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTCC	900
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

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5      TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTTGA GATTGAWACT      50
      CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC      100
      CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA      150
      AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT      200
10     TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC      250
      AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG      300
      TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC      350
      GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCCGGTGG      400
      TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAGTTGATT AACAAACATTG      450
15     CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC      500
      AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA      550
      CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCCGGTCAA ATGAACGAAC      600
      CACCTGGAGC TAGAGCCAGA GTTGCCCTTGA CCGGTTTGAC TATCGCTGAA      650
      TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT      700
20     TTTCAGATT ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA      750
      TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG      800
      TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCGGTTA CCTCCGTCCA      850
      AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA      900
      CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCCAGAGG TATCTCCGAA      950
25     TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT      1000
      GGACGCTGCC GTTGTCGGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC      1050
      AACAACTTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG      1100
      GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG      1150
      AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTC      1200
30     CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC      1250
      AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTTG      1283
  
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35 2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 1287 bases
      (B) TYPE: Nucleic acid
40     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*
 (B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

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50     CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA      50
      ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC      100
      ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA      150
      AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCCAGTT GGTAGAGGTA      200
55     CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT      250
      CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT      300
      CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAAACTGGT ATTAAGGTTG      350
      TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCGGT      400
      GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT      450
60     YGCAAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA      500
  
```

	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATGTCAG	650
	AATATTTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTTCGCC	CACTTGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

20 2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTGCG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
40	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACTGAAGCT	GAAGTTTTTG	AAACCGGTAT	TAAGGTGTGC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTTC	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CAACCAAGAAG	GGTTCCGTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTCGCCCA	CTTGATGCT	ACCACCGTCT	TGCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTCGCT	GTTGTCGGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCCTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250

5 2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20 AGGTGCCTCT GTCACTGACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTT GAACAATCCA CTTCTGCTGA AGTTTTGGAG ACTGGTATCA 200
25 AGGTTGTCGA CTTGTTGGCC CTTACGCCA GAGGTGGTAA GATTGGTTTG 250
TTCGGTGGTG CCGGTGTCGG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCACG GTGGTTTCTC TGTTTTCACT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
30 GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTTCGTT 550
GACAACATTT TCAGATTAC CCAGGCCGGT TCTGAAGTGT CTGCTTTGTT 600
GGGTCGTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
35 TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTTGGTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAACTTTG CAGCTTACAA GTCTTTGCAA GATATCATTG 950
40 CCATTTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTTGTCT CAACCATTCTG CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTTG GACGGTAAGT ACGACCACTT 1140

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2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTTAGGTGAA	100
5	AACACCGTCA	GAACCATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTA CTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTT	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTCGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	ACACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTA CTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAACCC	GGTATTAAAGG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGA C TGGT	TTGACCATTG	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCTG	GTTATCAACC	AACCTTGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTCTGATC	CATTGGATTC	CAAATCCAGA	1000
	TTGTTGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

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2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1285 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTGC	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACCTGGTGC	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCAACG	GTGACCCTGT	AGACGACCGT	250
	GGTCCCCTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGTC	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTACTIONGTA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCGGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCTGC	TTGGTGTTTCG	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCCGTG	CCCGTGTCTGC	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTCGTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCTT	TCCGCTGTCTG	GTTACCAGCC	TACCCTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCTGTC	900
	CACCACCTTC	GCCCATTG	ATGCCACCAC	TGTCTTGCTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTCTGACC	CTCTCGACTC	CAAGTCCCGT	1000
	CTTCTTGACG	CCGCTGTCTG	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAGGAT	ATCATTGCCA	1100
55	TTCTTGATAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCCAG	CCTTTCGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAGGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

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2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG	TCAATTGCCA	GCTATTTTGA	ACGCTTTTGA	AATCGACACT	50
CCAGAAGGAA	AGTTGGTTTT	GGAAGTCGCT	CAACATTTGG	GTGAAAACAC	100
TGTCAGAAC	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	CGTGGTGAAA	150
ACGTTTCTGA	CTATGGTGCT	CCAATTTCCG	TCCCAGTTGG	TAGAGAAACC	200
TTGGGTAGAA	TTATCAACGT	TATTGGTGAG	CCAATTGACG	AAAGAGGTCC	250
AATCAACTCC	AAGATGAGAA	AGCCAATTCA	TGCTGATCCT	CCATTATTTCG	300
TTGAACAATC	CACTGCTGCT	GAAGTTTTGG	AAACTGGTAT	CAAGGTTGTC	350
GACTTGTTGG	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
TGCCGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAATTGATT	AACAACATTG	450
CCAAGGCTCA	TGGTGGTTTC	TCTGTCTTCA	CTGGTGTCGG	TGAAAGAACC	500
AGAGAAGGTA	ACGATTTGTA	CCGTGAAATG	AAGGAAACTG	GTGTTATCAA	550
CTTGGAAGGT	GATTCTAAGG	TCGCGTTGGT	TTTCGGTCAA	ATGAACGAAC	600
CTCCTGGAGC	TAGAGCTAGA	GTCGCCTTGA	CTGGTTTGAC	CATCGCTGAA	650
TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTTA	TCGACAACAT	700
TTTCAGATTC	ACACAAGCCG	GTTCCGAAGT	GTCCGCTTTG	TTGGGTCGTA	750
TTCCATCCGC	TGTCGGTTAT	CAACCAACTT	TGGCCACCGA	TATGGGTTTG	800
TTGCAAGAAA	GAATTACTAC	CACCAAGAAG	GGTTCGTC	CTTCTGTCCA	850
AGCCGTTTAC	GTGCCAGCTG	ATGATTTGAC	TGATCCTGCT	CCAGCTACCA	900
CTTTCGCGCA	TTTGGATGCC	ACCACTGTGT	TGTCCAGAGG	TATCTCTGAA	950
TTGGGTATCT	ACCCAGCTGT	CGATCCTTTG	GATTCCAAAT	CTAGATTGTT	1000
GGATGCTGCC	GTCGTTGGTC	AAGAACATTA	CGATGTCGCT	ACTCAAGTTC	1050
AACAAACTTT	GCAAGCTTAC	AAGTCTTTGC	AAGATATCAT	TGCCATTTTG	1100
GGTATGGATG	AATTGTCCGA	ACAAGATAAG	TTGACCGTCG	AAAGAGCTAG	1150
AAAGATTCAA	AGATTCTTGT	CTCAACCTTT	CGCTGTCGCT	GAAGTCTTCA	1200
CTGGTATCCC	AGGTAGATTG	GTCAGATTAA	AGGACACCAT	CTCTTCTTTC	1250
AAGGCTGTCT	TGGACGGTAA	GTACGATCAC	TTG		1283

2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTCTG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCT	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTCCGGTGGT	400
	GCTGGTGTCT	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTAC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAT	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCGA	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATTC	GCTGTTGCCG	AAGTTTTTCAC	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

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2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

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|----|-----|----------------------|
| 35 | (A) | LENGTH: 1267 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|---------------------------------|
| | (A) | ORGANISM: <i>Candida utilis</i> |
| | (B) | STRAIN: Csp 388 |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	TGAGAGCCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCGA	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACG	GTGGTTTCTC	450
	TGTTTTTCACC	GGTGTCCGGT	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCC	GTGCCCCTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAAACATTT	TCAGATTCAC	CCAGGCCGGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCACT	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCTG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTCGAG	AGAGCCAGAA	AGATTCAGCG	TTTCCTTTCC	1150
	CAGCCATTCTG	CTGTCTGCTGA	GGTTTTTCACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTTG	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

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2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1296 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTCACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGAAAACC	GGTATCAAGG	350
40	TTGTCTGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGA CTGGT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTG GCC	ACCGATATGG	800
	GTCTTTTGA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTCTGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCTGCA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTG GCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

	TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
	AGAATGGTGA	CAACGACTTG	GTTTTGGAAG	TTGCCCAGCA	CTTGGGTGAG	100
20	AACACCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
	TGCGTCCGTC	AAGGACACTG	GCGCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
	GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
	GGTCCCATCG	AGCTGACCCA	GAGAAACCCT	ATCCACGCCG	ACCCCCCTC	300
	GTTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGGAGACT	GGTATCAAGG	350
25	TTGTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTGAGGAGT	TGATCAACAA	450
	CATCGCCAAG	GCCCACGGTG	GGTTCTCGGT	CTTCACTGGT	GTCGGTGAGA	500
	GAAGTAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
	ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTCG	GTCAGATGAA	600
30	CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTG	650
	CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTGGG	750
	TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGGA	ACTGATATGG	800
	GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
35	GTGCAGGCCG	TCTACGTCCC	CGTGATGAC	TTGACTGACC	CTGCTCCCGC	900
	CACCACCTTT	GCCCCTTGG	ACGCCACCAC	CGTGTTGTCC	AGAGGTATCT	950
	CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGACTC	CAAATCGAGA	1000
	TTGTTGGACG	CTGCCGTGGT	CGGTCAGGAG	CACTACGATG	TTGCCTCGAA	1050
	CGTCCAGCAG	ACCTTGACAG	CCTACAAGTC	CTTGCAGGAT	ATCATTGCCA	1100
40	TTTTGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
	GCCAGAAAGA	TCCAGAGATT	CTTGTCGCAG	CCCTTCGCTG	TTGCCGAGGT	1200
	TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
	CTTTCAAGGA	GGTTTTTGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

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2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

```

TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTA CTCCGTG      100
5  TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA      150
AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCGTGC CCGTGTTGCC      250
CTTACCGGTT TGACCATTCG TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
10 TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCACTCAA      400
GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCGG      450
TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA      500
CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                          534

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15

2) INFORMATION FOR SEQ ID NO: 480

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 494 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

```

CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
35 TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
GAGGGTGA CT CCAAGGTCGC CTTGGTCTTC GGTGATGA ACGAGCCCCC      250
TGGAGCCCGA GCCCGAGTCG CTTGACCGG TTTGACCATT GCCGAATACT      300
TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTTCATTGA CAACATTTTC      350
40 CGATTACCC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC      400
CTCCGCCGTC GGTTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC      450
AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC              494

```

45

2) INFORMATION FOR SEQ ID NO: 481

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 415 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

295

	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTCGG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACCTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCGG	TTACCAGCCC	350
	ACCCTCGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

2) INFORMATION FOR SEQ ID NO: 482

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1281 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Geotrichum* spp.

(B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAGC	TCGTTCTCGA	GGTTGCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTAAGGAGG	TCTCGTCCGT	GGTCAGCCCC	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATT	CCGTTGGTGC	TGGTACTCTT	200
	GGTAGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	TCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTCGAT	350
	CTCCTTGCCC	CCTACGCCCC	TGGTGTAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTTT	TCATTTCAGGA	GCTGATTAAC	AACATTGCCA	450
	AGGCCCATGG	TGGTTTCTCC	GTTTTACCG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCG	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCC	TGCCCGTGTT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGTTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATT	750
45	CCTCCGCTGT	CGGTTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACTT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCCC	GCTACCACCT	900
	TCGCCCATTT	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGA	1000
50	TATCACCCTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCC GTAA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	ACACTGTTTC	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

2) INFORMATION FOR SEQ ID NO: 483

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

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15  ATTCAAGAAT TGATCGTACG TTCCTCCGCC CCACACACGA TCAATGGAGA      50
    AAGAAACAAA TTTTGTGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA      100
    ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTTAC TGGTGTTCGGC      150
    GAGCGGACCC GTGAAGGAAA TGAATTGTAC CACGAAATGC AGGAAACCCG      200
    TGTTATCCAG CTCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA      250
20  TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC      300
    GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA      350
    TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC      400
    TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG      450
    TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCACCCCT      500
25  CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACCACCT ACCACCAAGG      550
    GCTCCATCAC CTCTGTGTCAR GCCGTCTACG TCCCCG      586
  
```

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

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45  GCGTGGCCAG AAGGTCATTG ACACTGGTGC TCCCATCACC ATCCCCGTGC      50
    GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC      100
    GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC      150
    CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA      200
50  TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT      250
    CTGTTCCGGT GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT      300
    CAACAACATC GCCAAGGCCC ACGGTGGTTC CTCCGTGTTT ACTGGTGTCTG      350
    GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT GATTGAAACC      400
    GGTGTCATTA ACCTCGAGGG TGAATCGAAG GTGGCTCTGG TGTTCGGTCA      450
55  GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA      500
    CTGTGGCCGA GTACTTCCGT GACGACGAGG GCCAGGATGT GCTGCTGTTC      550
    ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCGGAGA CTTCCGGCTCT      600
    GCTGGGTCGT ATCCCTTCGT CGGTGCGGTTA CCAGCCCACT TTGTCGACCG      650
    ATATGGGTGC CATGCAGGAG CGTATCACCA CCACCAAGAA GGGTTCGATT      700
60  ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC      750
  
```

	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTCGC	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

10

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1261 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTCTGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCCG	TAACGGTACC	TTGGGCCGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTTCG	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGTGG	TGCYGGTGTY	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCCG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCGGTTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCCGT	GTCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCCGAGAC	TTCCGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCA	900
	CTTGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCYGAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCCGA	GGAGGACAAG	CTCACTGTCTG	AGCGTGCCCG	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTC	1250
	TGTCCGGTAA	G				1261

55

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1282 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAAGT	TGGTCTTGGA	GGTGGCCCAG	CACTTGGGTG	AGAACACCGT	100
15	CAGAACCATT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
	TCACCGACAC	YGGTGCCCCT	ATCTCCGTGC	CTGTCGGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTCACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGGAGA	CTGGTATCAA	GGTTGTCGAC	350
20	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAAC	AACATTGCCA	450
	AGGCCACCGG	TGGTTTCTCC	GTTTTCACCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTCG	CCTTGTTTTT	CGGTCAGATG	AACGAGCCTC	600
25	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTTCGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
30	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
	TCGCCCACTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCTGA	CCCCTTGAC	TCCAACCTCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGCAGG	ATATCATTCG	CATTTTGGGT	1100
35	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTTAC	1200
	CGGTATTGAG	GCTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

40

2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 482 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: WSA-214

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAGAACAAC	ATTGCCAAGG	CTCACGGTGG	100
60	TTACTCTGTC	TTCACTGGTG	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150

TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200
AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCGG	GTGCCCCGTGC	250
CCGTGTCGCT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
5 GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCCCT	CTGCCGTCGG	400
TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

TCGAACAAGG	TAACTTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTTCGTGGTG	150
30 AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTCGG	400
35 TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
TAACTTGGA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
AACCACCAGG	TGCTAGAGCT	CGTGTTGCTT	TAACTGGTTT	GACCATTGCT	650
40 GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
GTATTCCATC	TGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCAG	TTACTTCTGT	850
CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
45 CCACTTTCGC	CCATTTGGAT	GCTACTACTG	TCTTGTCTCG	TGGTATTTCA	950
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
50 AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

55

2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1291 bases
 (B) TYPE: Nucleic acid

300

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTCGAA	CAAGGTAAC	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTTTAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG	150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC	200
	GTGAAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA	250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC	300
	TTCATTCACT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA	350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA	400
20	TTCGGTGGTG	CCGGTGTCTG	TAAAACGTGC	TTTATCCAAG	AATTGATTAA	450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTCACC	GGTGTGGGTG	500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAACTGGT	550
	GTTATTAAC	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT	600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA	650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT	700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAAGTT	CTGCCTTATT	750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA	800
	TGGGTTTGT	ACAAGAACGT	ATTACCACCA	CACAAAAGG	TTCAGTTACT	850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC	900
30	AGCTACCACT	TTCGCCCATT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA	950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGTCT	ATCCATTAGA	TTCTAAATCA	1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC	1050
	CAACGTTCAA	CAAACTTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG	1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GACTGTGCGA	1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTG	CTGTTGCCGA	1200
	AGTTTTCAC	GGTATCCCAG	GTAGATTGGT	TAGATTAAAA	GACACTATCA	1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A	1291

40

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 508 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
(B) STRAIN: ATCC 10658

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCTTA	CAGCAAGCTT	ATAAAGGAGC	50
	GAAAAAGATC	TGACATTCGG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA	150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG	200

301

TCATT	CAGCT	CAAGA	ACGAC	AAGT	CCAAGG	CCGCT	CTGGT	CTTC	GGACAG	250
ATGAA	CGAGC	CCCC	CGGAGC	TCGT	GCCCCG	GTCG	CTCTGA	CCGT	CTCAC	300
CATCG	CCGAG	TACT	TCCGTG	ACGT	CGAAGG	ACAG	GATGTG	CTAC	TCTTCA	350
TCGAC	AACAT	TTTCC	GATTG	ACCC	AGGCCG	GTTCA	GAGGT	ATCT	GCCCTG	400
5	CTCGG	ACGTA	TCCCAT	CTGCTG	TGTC	GGATAC	CAGCCC	CACAC	TCTCA	450
	TATGG	GTTGGT	ATGCA	AGAGC	GAAT	CACAAC	CACCA	AAGAAG	GGTTC	500
	CCTCC	GTC							GATTA	508

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2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 686 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhodotorula mucilaginosa*
 (B) STRAIN: ATCC 66034

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

TGTCCT	CATT	CAGGAG	CTCA	TCAACA	AACAT	CGCCA	AAGGCC	CACGGT	GGTT	50
ACTCGG	TCTT	CACCGG	TGTC	GGCGAG	CGTA	CCCGT	GAGGG	TAACGG	TGAG	100
TCTCCCC	CCTT	CAAAC	TTTTG	GCCGG	CTAGT	TGGCG	CAGCG	CAAAC	TGACG	150
30	CGCGC	GCCC	CT	GTCCAG	ACTT	GTACC	ACGAG	ATGAT	CGAGA	200
	CCAGCT	CGAG	AACGACA	ACT	CGAAG	TGCGC	TCTCG	TGTT	CGCCAG	250
	ACGAG	CCCC	TGGT	GCCCCG	T	GCCCCG	TGTCG	CTCTC	ACTGG	300
	TCTCT	CTCTC	GAGCG	TCCCTG	GCTTG	AACG	CTGAC	ACGTC	ACGCA	350
	GTCTC	ACTAT	TGCTG	AGTAC	TTCCG	TGACG	AGGAG	GGG	CCCA	400
35	CTCTT	CATCG	ACAAC	ATCTT	CCGTT	TCCAC	CAGGG	TGAGC	CGCCT	450
	GGCATT	CTCC	CGTTT	CTTT	GCGCT	GACGT	CTGT	CCCCG	TAGCC	500
	GGAGG	TGCT	GCCCT	TCTCG	GACGT	ATCCC	GTCCG	CTGTC	GGATA	550
	CGACT	CTCTC	GACCG	ACATG	GGTC	AGATG	AGGAG	CGTAT	CACGT	600
	TGGCC	GCAGC	TCCGT	CCGCG	GCGCC	CTTTG	TGTCT	GACCG	TGTTCC	650
40	CTCAG	CACCA	CCAAG	AAGGG	CTCGA	TACC	TGTGTC			686

45 2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60	TGTCTT	GATT	CAGGAG	CTCA	TCAACA	ACGT	CGCCA	AAGGCG	CACGGT	GGTT	50
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	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCCTGCCCC	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTAATTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCC	TCCGCTGTCTG	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTTCGCCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

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2) INFORMATION FOR SEQ ID NO: 493

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1211 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: WSA-148

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTCGGCCC	CGGTACCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCAT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACGAGCTGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTCGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCCACG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTTCAGCT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGTT	450
	CGGTTCAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCCGTGTC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCGCTGAC	800
	GATCTGACGG	ATCCCCGCCC	CGCCACCACC	TTGCCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCGAGGTA	TCTCTGAGCT	GGGTATCTAC	CCCCTGTCTG	900
	ACCCCTCTGA	CTCCAAGTCG	CGTATGCTGG	ACCCCGGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTTCGCGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

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2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

```

TCTTGTTAGA GGCACCCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC      50
CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA      100
ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC      150
20 TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA      200
CCGGTATTAA GGTGTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG      250
ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA      300
GCTTATTAAC AACATTGCTA AGGCCACGGT TGGTTACTCT GTCTTCACTG      350
GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG      400
25 GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT      450
CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG      500
GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG      550
TTGTTCAATTG ACAACATTTT CCGATTACAC CAGGCCGGTT CTGAGGTCTC      600
TGCCCTTGTTG GGTCGTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG      650
30 CTA CTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAGGGT      700
TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA      750
TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT      800
CCC GATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCCTCTTGGT      850
TCCAAGTCCC GTCTTTTGGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA      900
35 CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG      950
ATATCATTCG CATTTTGGGT ATGACGAAT TGTCTGAGGC TGATAAGCTC      1000
ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC      1050
CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG      1100
ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG      1133

```

2) INFORMATION FOR SEQ ID NO: 495

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

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GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG      50
60 GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTTC      100

```

	AGTATTAATT	GTTTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCCG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCCGT	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAATTTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCATCTCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGGTC	GTATCCCATC	TGCCGTCCGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTTTATTCAA	GAATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTGC	AAAGGCTCAT	GGTGGTTACT	100
	CCGTGTTTAC	TGGTGTCCGC	GAGCGAACTC	GTGAGGGTAA	CGACTTGTAC	150
	CACGAAATGC	AGGAGACCTC	TGTCATTGAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAAA	TGAACGAACC	TCCTGGTGCT	CGTGCTCGTG	250
	TTGCTCTGAG	TGGGTAAGTT	GTTCTTTCGC	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGTCT	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTTCTTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGGT	550
	GTGAGAAGTG	CGCCGGAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTCAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTCGTATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGGAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

```

5      TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
      CCGTCGGCCG AGGTACCCTT GGTCTGAATCA TCAACGTCTG TGGTGAGCCC      100
      ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC      150
      TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA      200
10     CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG      250
      ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA      300
      GCTGATTAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG      350
      GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG      400
      GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT      450
15     CGGTCAGATG AACGAGCCTC CCGGAGCCCG TGCCCGAGTC GCCCTTACTG      500
      GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG      550
      CTCTTCGTTG ACAACATTTT CCGATTACAC CAGGCCGGTT CCGAGGTGTC      600
      CGCTCTGCTT GGTCGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG      650
      CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT      700
20     TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA      750
      TCCTGTCTCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCCTGT      800
      CCGGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT      850
      TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA      900
      TGTTCGTTCC AACGTCCAGC AGACCCTCCA GGCTTACAAG TCTCTCCAGG      950
25     ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG      1000
      ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC      1050
      CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG      1100
      AACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC      1148
  
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30

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

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35     (A) LENGTH: 966 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

```

      GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
      CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC      100
50     CCAGACTCGT GAGCATTTGC TGCTCGCCC CGAGGTTGGT GTCCAGAAGA      150
      TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG      200
      GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA      250
      GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGTCTCTGT GCTCTCGAAG      300
      GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT      350
55     GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT      400
      GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT      450
      CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTGAGATT      500
      GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC      550
      CTTCAAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC      600
60     TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCAATTGCT      650
  
```

GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700
CCTGACCGAG	GCGGAGGGTG	GTCGTCGTAC	TGGCTTCGGT	GCCAACTACC	750
GTCCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTTCCCGCA	CACCGTGTCC	800
AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
5 TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
GCTGGTCAAC	GCTTCA				966

10

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTAAAGCA	CATTGTTGTT	100
TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAACCTGT	150
30 CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
ATACATTCCT	ACCCCAGTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTAAGTTGAA	CACTGGACGT	400
35 GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
AGGAACCTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
GGTGTTAAGC	GTGAAGACCT	TAAAGCGTGGT	ATGGTTGTTG	CTAAACCAGG	600
TACCGTTAAG	CCACACACCA	AGTTCCTTGC	CTCCATCTAT	GTTTTGACTA	650
40 AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACTA	CAGACCTCAA	700
CTTTTCCTTG	GTTCTGCTGA	TGTTACCACT	GTCTTGACCT	TCCCAGAGGG	750
TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
GCGAACTTGT	TCACCCAGTT	GCTGTGCAAC	AAGGCCAACG	TTTCAA	846

45

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

	GGTGCCATTA	TTGTTGTTGC	TGCCTCTGAT	GGACAGATGC	CCCAGACCCG	50
	TGAGCATCTT	TTGCTTGCCC	GCCAAGTCGG	TATGCAAAAG	GTCGTTGTGT	100
5	TTGTTAACAA	GATTGATACC	ATTGATGACC	CTGAAATGCT	TGATCTTGTC	150
	GAGATGGAGA	TGCGTGAAC	GTTGAATGAA	TATGACTTCG	ATGGAGATAA	200
	CTCTCCTGTC	ATTATGGGCT	CTGCTCTTGC	TGCTCTTGAG	GACAAGAACC	250
	CCGAGATTGG	TAAGGACCGT	ATCATGCAGC	TCTTGACGCG	TGTTGATGAA	300
	TGGATCCCTA	CCCCCGAGCG	TGACCTTGAC	AAGCCTTTCA	TGATGCCTAT	350
10	TGAGGCCTCT	TTCTCCATTT	CTGGTCGTGG	TACTGTTGCC	ACTGGCCGTG	400
	TCGAGCGTGG	TATTCTCAAG	AAGGGTGAGG	AAGTCGAGAT	CGTTGGTTTC	450
	AACAAGCAGC	CCCTGAAATC	TGTTGTTACT	GGTATTGAAA	TGTTCAAGAA	500
	GGAACCTGAT	CAGGCCCAGG	GCGGTGATAA	TGCTGGTATC	TTGCTTCGTG	550
	GTATTCGTCTG	TGAGGACTTG	CAGCGTGGTA	TGGTTTTGGC	CAAGCCTGGA	600
15	ACTGTTAAGG	CTCACACCAA	GTTCCCTTCC	TCCATCTACG	TTCTCTCCAA	650
	GGAAGAGGGC	GGCCGTCACT	CTCCTTTCCG	TATGAACTAT	CGTCCCCAGA	700
	TGTTTCGTTTC	TGCAGCTGAT	GTCACCGTTA	CTCTTACTTT	CCCTGAGGGT	750
	GTTGAACAGC	ACACTCAGGT	CTTCCCTGGT	GAGAACACCG	AGATGGTTGG	800
20	CGAGCTCGTT	CACCCTACTG	CTATTGAGGT	TGGTCAACGC	TTCAAC	846

2) INFORMATION FOR SEQ ID NO: 501

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 944 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*

35 (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

	AGTTGTCGTC	GTTGCTGCTT	CAGACGGTCA	AATGTATGCA	ACCGAGAGCA	50
40	CTCCCGGATC	TTGGTTTAAA	TGGCACTAAT	ATAAGACAGG	CCTCAAACCTC	100
	GAGAGCATTT	ACTTCTCGCC	CGTCAGATCG	GTATCCAAAA	AATCGTCGTC	150
	TTCGTGAACA	AGGTTGATGC	CATCGAGGAC	AAAGAGATGT	TGGAGCTTGT	200
	TGAATTGGAG	ATGCGTGAAC	TCCTAACCAG	CTACGGTTTC	GAGGGTGAAG	250
	AAACTCCCAT	CATTTTGGC	TCTGCTCTCT	GTGCCCTCGA	AGGAAGACAA	300
45	CCCGAGATCG	GTGTTACCAA	GATTGATGAG	CTCTTGACAG	CCGTCGACAC	350
	CTGGATTCCC	ACTCCTCAGC	GTGAGACTGA	CAAGCCCTTC	TTGATGTCCA	400
	TTGAGGAAGT	GTTCTCTATT	TCCGGACGAG	GAACCGTTGT	CTCCGGCCGT	450
	GTGGAGCGTG	GTATCCTCAA	GAAGGACTCC	GAAGTTGAAA	TTGTCGGCGG	500
	TTCGCCCGAG	CCAATCAAAA	CCAAGGTTAC	CGATATCGAA	ACCTTTAAGA	550
50	AGTCTTGCGA	CGAGTCTCGC	GCTGGTGATA	ACTCCGGCTT	GCTCCTACGA	600
	GGCGTTAAGC	TGAAGATAT	TAGCCGTGGC	ATGGTCGTCG	CTGTACCAGG	650
	AAGTGTCAAG	GCCCATACTG	AATTCTTAGT	TTCGCTTTAC	GTCCTCACCG	700
	AAGCTGAGGG	TGGGCGCAAA	TCTGGATTCA	GCAGCAAGTA	CCGCCACACG	750
	ATGTTCAATC	GCACTGCCGG	TATGTAATAC	TGTGATAATT	TCGTTGACAT	800
55	GGTACTGATT	GAATTCTATA	GACGAAGCGG	CTCAGCTCAG	CTGGCCCGGA	850
	GAAGATCAAG	ACAAGATGGC	TATGCCAGGA	GACAATATCG	AAATGATTTG	900
	CACCACCTTG	CACCCAGTTG	CCGCCGAGGC	TGGCCAGCGA	TTCA	944

60

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

GCTATCATCG	TCGTTGCTGC	CTCCGATGGA	CAGATGCCCC	AGACCCGTGA	50
ACACTTGCTC	CTCGCTCGTC	AGGTCGGTGT	CCAGCGAATT	GTCGTCTTCG	100
TCAACAAGGT	CGATGCCATT	GATGACCCCG	AGATGCTTGA	GCTCGTCGAG	150
ATGGAGATGC	GCGAGTTCT	TAACACCTAC	GGCTTCGAAG	GCGACGACAC	200
TCCCGTCATC	ATGGGCTCTG	CTCTTATGTC	TCTCCAGAAC	CAGCGCCCCG	250
AGATTGGCAC	CGAGAAGATC	GATGAGCTCC	TTGCTGCCGT	CGACGAGTGG	300
ATCCCAACCC	CCGAGCGTGA	CCTTGACAAG	CCCTTCCTTA	TGTCCGTCTGA	350
GGATGTCTTC	TCCATTGCCG	GCCGTGGTAC	CGTCGTGTCT	GGCCGTGTGG	400
AGCGTGGTAT	TCTGAAGCGT	GATCAGGAGA	TCGAGCTTGT	CGGAAAGGGG	450
CAGGAGGTTA	TCAAGACCAA	GGTTACCGAC	ATTGAGACCT	TCAAGAAGTC	500
TTGTGAGCAG	TCCCAGGCTG	GTGACAACCT	TGGTCTCCTC	ATCCGAGGTG	550
TTCGCCGTGA	GGATGTCCGC	CGTGGTATGG	TTGTCTGCGC	TCCTGGCACC	600
GTCAAGTCTC	ATACCCAGTT	TCTCGCTTCC	CTCTACGTCC	TCACCAAGGA	650
GGAGGGTGGC	CGACACACCG	GTTTCCAGGA	GCACTACCGA	CCCCAGCTCT	700
ATCTCCGAAC	TGCAGATGAG	TCCATTGACC	TGACTTTCCC	CGAGGGTACT	750
GAGGATGCCT	CCAGTAAGAT	GGTCATGCCT	GGTGACAACA	CCGAGATGGT	800
TGTCACCATG	GGTCACCCCA	ATGCCATCGA	GGTTGGTCAG	CGATTCAAC	849

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

TGGTGCTATT	GTCGTTGTTG	CTGCTGCTGA	CGGCCAAATG	TAAGACGCCG	50
CGAGGGACTG	CTGAGGGTTT	TATGCTTTTT	AGGCCCCCTT	GTTTCTGAGA	100
GCATGATGAT	ACTAATATTC	GGAAACGTAT	CTATTAGGCC	TCAAACACGT	150
GAGCATTTGC	TCCTTGCCCC	ACAGGTCGGT	GTCCAAAAGA	TCGTCGTTTT	200
CGTGAACAAA	GTCGACGCCC	TTGAGGACAA	GGAGATGTTG	GAGCTTGTCG	250
AGTTAGAAAT	GAGAGAGCTC	TTAAACACCT	ACGGCTTCGA	GGGTGAAGAG	300
ACACCCATCA	TCTTTGGTTC	TGCCCTTTGC	GCCATGGAAG	GCCGTGAGCC	350
TGAGTTGGGA	GAAAAGAAAA	TTGATGAATT	GCTGGAGGCT	GTTGATACTT	400

	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT ¹	458
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTGAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAAGTG	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCTTGCCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTCGGC	CAGAACTATC	GTCCTCAAAT	800
	GTTTCATCCGC	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAACCTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
15	CGGCCAGCGA	TTCA				1064

2) INFORMATION FOR SEQ ID NO: 504

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	GCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAGTC	150
	GGTGTTGAGA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TCGAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGGATA	CTTGGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTCGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTCAT	800
50	TCTTTCACTA	TATTCCTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTG	ATGCCCGGTG	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982
55						

2) INFORMATION FOR SEQ ID NO: 505

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 931 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCTCA	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATAACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCGTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GA CTGAGGCT	700
	GAAGGTGGTC	GTCGTA CTGG	ATTCGGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTACT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCAGT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTA ACTTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAA ACT	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500

	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550
	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
5	TTATTTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTTAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTC	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 964 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
30	GGTCGTTTTT	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAACCTC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
35	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCGGAC	GTCGAAATTG	500
	TTGGTGGCTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAACT	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
40	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGATTT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTTCA	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
45	GACAACGTCG	AGATGATTTG	CAAAACCCTC	CACCCCATTT	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

50 2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

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5  GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTCGAAGC CCCAGACCCG      50
   AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT      100
   TTGTTAACAA GGTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT      150
   GACATGGAGA TGCAGATCT GCTGACCCAG TACGGTTTGT ATGGTGACAA      200
10  CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA      250
   AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG      300
   CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCGT      350
   TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG      400
   TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTTGGCTAC      450
15  AACACAAGC CCATCAAGGC TGTGTGTACC GGTATTGAGA TGTTCAAGAA      500
   GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG      550
   GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC      600
   ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC      650
   CGAGGAGGGT GGTCGAACCA GCTCTTTCGG CGCCAACTAC CGACCCGAGA      700
20  TGTTTCATCCG AACTTCTTCC GTCACCGCCA CTCTCACCTT CCCCAGAGGT      750
   ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT      800
   CGAGCTTGTT CACCTTACCG CCATTGAGGT CAACCAGCGA TTCA          844

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25

2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:

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30  (A) LENGTH: 1067 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

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   CTTGGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA      50
   CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC      100
   CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC      150
45  CGATGTTGCT ATGCTTGTCG TGCCCGCCGA GGCTGGTGGT TTCGAAGCTG      200
   CTTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC      250
   CTTGGTGTCA AGCAGATCAT TTGCGCCATC AACAAGATGG ACAAGTGCGA      300
   CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC      350
   TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC      400
50  GGTTTCATGG GTGACAACAT GGTGAGCGC TCCACCAACA TGCCGTGGTA      450
   CAAGGGCAAG ACCTTGGTCG AGGCCCTCGA CATGATGGAG CCCCCGAAGA      500
   GGCCCGTCGA CAAGCCCTG CGTCTTCCCC TCCAGGGTGT GTACAAGATC      550
   GGTGGTATCG GTACCGTCCC TGTCGGTCGT GTGGAGACTG GTCAGTCAA      600
   GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA      650
55  AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC      700
   AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG      750
   TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCCT      800
   TCACCGCCCA GGTCATCATC TTGAACCACC CTGGTACCAT CAAGGCCGGT      850
   TACTCCCCTG TGGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA      900
60  CGAGATCACC AGCCGTATGG ACAAGCGTAC CGGTAAGGCC CTTGAGGAGA      950

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ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000
TGCAAGCCCA	TGGTCGTCTGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCG	1050
TTTCGCCGTG	CGTGACG				1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA	ACGTGGTATT	ACTATTGATA	TTACCTTATG	GAAGTTCGAG	50
ACCACCAAGT	ACTACTACAC	CGTCATTGAT	GCCCCTGGTC	ACCGTGACTT	100
25 CATCAAGAAC	ATGATTACGG	GTACTTCTCA	AGCCGATGTT	GCTATGCTTG	150
TTGTACCAGC	TGAGGCTGGT	GGTTTCGAGG	CCGCTTTCTC	CAAGGAAGGA	200
CAGACCCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTTGGTG	TCAAACAGAT	250
CATCTGTGCC	ATTAACAAGA	TGGACAAGTG	CGACTACAAG	GAGGACCGTT	300
ACAGTGAAAT	CCAGAAGGAA	GTCCAGGGTT	ACCTCAAGAA	GGTCGGTTAC	350
30 AATATTGAGA	AGGTGCCCTT	CGTTGCCATC	TCCGGTTTCA	TGGGAGACAA	400
CATGGTTGAG	CGTTCCACCA	ACATGCCCTG	GTATAAGGGA	AAGACATTGG	450
TCGAGGCCCT	TGATCAGATG	GAACCCCCAA	AGAGGCCCGT	TGACAAGCEA	500
CTTCGTCTTC	CCCTCCAGGG	TGTCTACAAG	ATCGGTGGTA	TCGGTACCGT	550
CCCCGTCCGT	CGTGTTGAAA	CTGGTATGTT	GAAGGCTGGT	ATGATTCTAA	600
35 CCTTTGCTCC	TAACCCAATC	ACCACTGAAT	GCAAATCCGT	TGAAATGCAC	650
CACGAAACCG	TTGAGGTTGC	TTACCCCGGT	GACAACGTCG	GTTTCAACGT	700
AAAGAACGTT	TCTACTTCTG	ACATTGCGAG	TGGTCACGTT	GCCTCTGATT	750
CTAAGAACGA	CCCTGCCAAG	GCTGCTGTTT	CCTTCACTGC	CCAGGTCATT	800
GTGCTCAACC	ACCCTGGTAC	CATTAAGGCC	GGTTACTGCC	CCGTCGTCGA	850
40 TTGCCACACC	GCTCACATTT	CATGTAAATT	CGAAGAGATC	ACCAGCCGTA	900
TGGACAAGCG	TACCGGTAAA	TCTCTTGAGG	AAAACCCCAA	GACCATCAAG	950
AACGGTGACG	CTGCCATGGT	TGTGCTCAAG	CCAATGAAGC	CCATGGTTGT	1000
CGAATCCTTC	ACTGAGTATG	CTCCTCTTGG	TCGTTTCGCT	GTTTCGTGAC	1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCTG	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCGTGGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCGC	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCGG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCCA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
25	GCCGCTTCGC	TGTCCGCGAT				1070

2) INFORMATION FOR SEQ ID NO: 512

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
 - (B) STRAIN: HM1-IMMS
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTCATTAT	GGAAATTCTGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAAC TTCAC	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTATA	CACTCTTGGA	GTAAACAAA	250
	TGATTGTTGG	WGTAAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTCAGT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTCAAGT	ATTGGAAC TG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAAATATAT	950
TAAGAATGGA	GATTTCAGCAC	TTGTTAAGAT	TGTTCCAAC	AAACCACTTT	1000
GTGTTGAAGA	ATTTGCTAAA	TTCCCACCAT	TGGGAAGATT	TGCTGTTAGA	1050
5 GA					1052

2) INFORMATION FOR SEQ ID NO: 513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25	GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
	GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
	TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
	GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
	CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
30	TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTAAGTTCGA	300
	GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
	CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
	CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
	CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
35	CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
	TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCGGG	600
	ATGAAGGTCG	TCTTCGCCCC	GACGTCCCAG	GTCTCGGAGG	TCAAGTCCGT	650
	CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCGGG	GACAACGTCG	700
	GCTTCAACGT	CCGCGGGCTC	GCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
40	GTCGGGGACG	TGACGAACGA	CCCGCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
	CCAGGTCATC	GTCATGAACC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
	CCGTTCATCGA	CTGCCACACC	GCGCACATCG	CGTGCCAGTT	CCAGCTCTTC	900
	CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCGAGATGG	AGAACCCGCC	950
	CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
45	CCCTGTGCTG	CGAGACGTTT	AACGACTACG	CGCCCCTCGG	CCGCTTCGCC	1050
	GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

5
 ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG 50
 ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTCACGAT 100
 CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA 150
 CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC 200
 10 TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT 250
 TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAGATGG 300
 ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG 350
 GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG 400
 CTTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG 450
 15 ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG 500
 CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCTGCA 550
 GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCGTG GGGCGCGTGG 600
 AGACCGGCAT CATGAAGCCG GGCAGCGTGG TGACGTTTCG GCCCGCCAAC 650
 GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA 700
 20 GGCAGAGCCC GCGACAACG TCGGCTTCAA CGTGAAGAAC GTGTCGGTGA 750
 AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG 800
 AAGGAGGCGG CCGACTTCAC GGCGCAGGTG ATCGTGCTGA ACCACCCCGG 850
 CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA 900
 TTGCGTGCCG CTTGCGGGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC 950
 25 AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT 1000
 CGTGAAGATG GTGCCGCAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT 1050
 ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG 1098

30
 2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGCA 100
 TCATCGATGC GCCCGGCCAC CCGACTTCA TCAAGAACAT GATCACGGGC 150
 50 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 55 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGCCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA 650
 60 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700

	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	-750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
5	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTC					1104

10

2) INFORMATION FOR SEQ ID NO: 516

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 25 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
30	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTTCACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	KCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
35	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
40	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGGCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
45	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
50	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCGG					1106

55 2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

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10  TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
    GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTTCACGA      100
    TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
    ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
15  CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
    TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
    GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
    GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
    GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTTCG      450
20  GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
    GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
    AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG      600
    GAGACCGGCA TCATGAAGCC GGCAGCAGTG GTGACGTTTCG CGCCCGCCAA      650
    CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
25  AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGGTG      750
    AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
    GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
    GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
    ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
30  CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA      1000
    TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC      1050
    TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG      1099

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35 2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

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    TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
    GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTTCACGA      100
    TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
55  ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
    CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
    TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
    GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
    GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
60  GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTTCG      450

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	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTCACGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTCATC	AAGAATCATG	TCACCGGCAC	GTCGCAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGGCGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAAAC	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGCGCA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
	GGGCGCTTCG	CTGTGCGCGA	C			1071

55

2) INFORMATION FOR SEQ ID NO: 520

(i) SEQUENCE CHARACTERISTICS:

60

320

(A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

15	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTCACGATC	ATCGATGCGC	100
	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
20	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
25	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
	ATGAAGCCGG	GCGACGTGGT	GACGTTTCGCG	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
30	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTCGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

55	TCGTTCAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTCGAGTCG	CCCAAGTCGG	100
	TGTTACGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACCGGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTTCGAC	200
	GCAGGGTGGC	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
60	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCCG	400
	AGAAGGTGCG	CTTCATCCCC	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
	TGCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTCGC	650
	GCCCCGCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	750
10	GTGTCTGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCCG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACAGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTCGCAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	CTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
60	CGTCGG					1106

2) INFORMATION FOR SEQ ID NO: 523

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

	TACGCGTG	GGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
20	GATCGACATT	GC	GCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCC	GGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGAC	GCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCAT	CTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTT	GGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
25	GACGACAAGA	CGGT	GATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGT	ACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCT	CGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGT	TACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGT	GCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
30	AGGACGTGTA	CAAGAT	CGGC	GGTATCGGGA	CGGTGCCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGA </td <td>AGCC</td> <td>GGGCGACGTG</td> <td>GTGACGTTTCG</td> <td>CGCCCCGCCAA</td> <td>650</td>	AGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCCAA	650
	CGTGACGACT	GAGGT	GAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCG	ACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCCGGTG	750
	AAGGACATCC	GCCGT	TGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
35	GAAGGAGGCG	GCCGACTTCA		CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC		GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA		GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC		CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG		AAGCCGATGT	GCGTGAGAGT	GTTCAACGAC	1050
40	TACGCGCCGC	TGGGCCGCTT		TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCG						1105

45 2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
10	GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACACGA	TCATCGATGC	GCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGGCGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCGT	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGC C GCAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C		1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTCGC	AGGCGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCAGACCCGC	GAGCACGCGC	250
TGCTTGCTT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCgatCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCCGGTGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAACGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCCGCGAC	AACGTCCGCT	TCAACGTGAA	GAACGTGTCG	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	GGAAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGGAGAAGA	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTC AAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

2) INFORMATION FOR SEQ ID NO: 527

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

5	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTC	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCCTG	250
10	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAKGGATT	CCACTGAGCC	300
	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGGAACCM	500
15	CCCTGCTTGA	AGCTYTGGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
	AAACCCTTGC	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
20	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTCGTTCT	GGGAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
25	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGGTTCCTG	GCAAGCCCAT	1050
	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
	GTGAC					1105

30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

35	(A)	LENGTH: 935 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Trichomonas vaginalis</i>
(B)	STRAIN: ATCC 30001

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTCGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCTTC	ACACTCGGCA	TCAAGCAGGT	CATTGTGCGC	GTCAACAAGA	150
50	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTTCGAC	AAGCCACTCC	GTCTTCCACT	400
55	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTAACTT	CGCCCCATCC	500
	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGCTCTT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGGC	TACGTCGTTG	GTGATACAAA	GCGTGACCCA	650
60	CCAGTCGAAT	GCGCTTCCTT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700

	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCGSCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTGAGAAAGG	ATGATGCCGC	850
	TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTCGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

2) INFORMATION FOR SEQ ID NO: 529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
	GAAATTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAGTGCG	500
35	TCCGAGCGAC	AAGCCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTCTGT	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
	ACGTCGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCCG	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

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5   TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA      50
    CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG      100
    CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG      150
    AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG      200
10  CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC      250
    GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCGCCG      300
    AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA      350
    GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT      400
    TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC      450
15  AACGTGGCCA AGGGCCACGG TGGTTTCTCC GTGTTCGCCG GCGTTGGCGA      500
    GCGCACCCGC GAGGGCACGG ATCTGTACCT GGAGATGATG CAGTCGAAGG      550
    TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG      600
    AACGAGCCCC CGGGTGCGCG TGC CGCGTGTT GCGCAGTCTG CGCTGACGAT      650
    GGCGGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTTCATCG      700
20  ACAACATCTT CCGCTTCACC CAGGCCAACT CCGAGGTGTC CGCCCTGCTG      750
    GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT      800
    TGGTATGCTG CAGGAGCGCA TTACGTGCGA GACGAAGGGC TCGATTACGT      850
    CTGTGCAGGC CGTGACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG      900
    GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT      950
25  TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGC CGCGTCGC      1000
    GTATCATGGA CCCC GATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
    GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTTGC      1100
    CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGGTGGACC      1150
    GCGCTCGCAA GGTGACGCGC TTCCTGTCGC AGCCGTTCCA GGTGGCCGAG      1200
30  GTGTTACCGG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA      1250
    GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA      1297
  
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35 2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 1298 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

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50  CTTCTCGGAG GGCGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG      50
    ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC      100
    GCGAACACGG GCCGCTGCAT TGC GATGCAG ACGACGGACC TGCTGAAGCT      150
    GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
55  GTGAGACGCT GGGCCGCATC TTCAAYGTTT TGGGCGACGC GATCGACCAG      250
    CGCGGCCCCC TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
    GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
    AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG      400
    TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
60  CAACGTCGCG AAGGGCCACG GCGGTTTCTC CGTGTGTTGCC GGC GTTGCGC      500
  
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	AGCGCACGCG	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
5	GACAACATCT	TCCGCTTCAC	GCAGGGCAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTTCG	ACGACCAGAT	CCCGGAGA	1298

20 2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTGCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CCGGTGC GCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCAGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTTCG	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTGCG	AGCCGTTCCA	GGTTGCGGAG	1200
60	GTGTTACGCG	GCATGACGGG	CCACTACGTG	CAGCTGGTGC	ACACGGTGGA	1250

GTCGTTCTCT GGCCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA

1297.

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
 GCGAACACCG GCCGCTGCAT TCGCATGCAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CCTCATCTCT CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GCGTGTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCAGTCT GCGCTGACGA 650
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
 GGGCCGCATT CCGGCCGCGC TGGGCTACCA GCCGACGCTT GCCGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCAG 850
 TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
 CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
 40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
 CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
 CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA 1200
 45 GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

330

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

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5  CTTCTCGGAG GGC GTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG      50
   ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
   GCGAACACCG GCCGCTGCAT TGC GATGCAG ACGACGGACC TGCTGAAGCT      150
   GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10  GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
   CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
   AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
   AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
   TTCGGCGGGT CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15  CAACGTTCGG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG      500
   AGCGCACGCG CGAGGGCACG GACCTATAAC TGGAGATGAT GCAGTCGAAG      550
   GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
   GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA      650
   TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC      700
20  GACAACATCT TCCGCTTAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
   GGCCCGCATT CCGGCCGCGG TGGCTTACCA CCGGACGCTT GCCGAGGATC      800
   TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
   TCCGTGCAGG CCGTGTACGT GCCGCGGGAT GATATCACTG ATCCCGCGCC      900
   CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25  TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTGC      1000
   CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
   GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
   CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
   CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA      1200
30  GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
   AGTCGTTCTC TGGCCTGCTG ATGGGGTTCG ACACCAGAT CCCGGAGA      1298

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35 2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1301 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

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50  GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
   AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
   GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
   GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55  GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC      250
   CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
   CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
   TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
   CTGTTTCGGC GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
60  CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500

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	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCA G TCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTA CT TCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCCGC	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTC	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	GCGAGACGCT	GGGTGCGATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTT	CGTGTTTGCT	GGCGTGGGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTGCGATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGC GG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCACT GGCATGACGG GTCACCTACGT TCAGCTGGAG GACACGGTGG 1250
 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

5

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGAC 100
 GCGAACACCG GCCGCTGCAT TGCATGCAG ACGACGGACC TGCTGAAGCT 150
 25 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 GTGAGACGCT GGGCCGCATC TTCAACGTTC TGGGCGATGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 30 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 CAATGTCGCG AAGGGCCACG GTGGTTTCTC CGTGTTTGCC GGC GTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
 35 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700
 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCTGTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA CCGGACGCTT GCGGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCAGTCTGA CAACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
 40 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTGC 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
 45 CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA 1200
 GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCTG ACGACCAGAT CCCGGAG 1297

50

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

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TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA      50
CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
10 AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CGGTGGGCCG      200
TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
GCGGCCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCG      300
AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGAAG ATCGGCCTGT      400
15 TTGGTGGCGC CGGTGTGGGC AAGACCGTGA TCATCATGGA GTTGATTAAC      450
AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTGTA CGGGCAGATG      600
AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT      650
20 GCGGGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTTCATCG      700
ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TGCCTGCTG      750
GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CGGAGGATCT      800
TGGTATGCTG CAGGAGCGCA TCACGTCGAC GACGAAGGGG TCGATCACGT      850
CCGTGCAGGC CGTGACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
25 GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
GGCGGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TGC GCGTCGC      1000
GTATCATGGA CCCCATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC      1150
30 GCGCGCGCAA GGTGACCCGG TTCCTGTGCG AGCCGTTCCA GGTTCGCGAG      1200
GTGTTACACG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA      1250
GTCGTTCTCT GGGCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA      1297

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35

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

20 GTKGAAATGT TCCGCAAGCT GCT

23

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

35

CGGAARTAGA ACTGSGGACG GTAG

24

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

50

ATCTTAGTAG TTTCTGCTGC TGA

23

55

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

60

335

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

40

CCRCGICCGG TRATGGTGAA GAT

23

2) INFORMATION FOR SEQ ID NO: 547

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55

GTACAGTTGC TTCAGGACGT ATC

23

60 2) INFORMATION FOR SEQ ID NO: 548

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTTCGATT TCATCACGTT G

2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA

2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG

2) INFORMATION FOR SEQ ID NO: 551

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

GAAGAAAAAA TCTTCGAACT GGCTA

2) INFORMATION FOR SEQ ID NO: 552

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

TACACGGCCG GTGACTACG

19

2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCTTACA TCGTTGTTTT TCTC

24

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA

24

2) INFORMATION FOR SEQ ID NO: 556

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

20

CGGCGCNATC YTS GTTGTG C

21

2) INFORMATION FOR SEQ ID NO: 557

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

35

CCMAGGCATR ACCATCTCGG TG

22

2) INFORMATION FOR SEQ ID NO: 558

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYG CITGGGT

20

2) INFORMATION FOR SEQ ID NO: 559

55

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

CCGACRGCRA YIGTYTGICK CAT

23

2) INFORMATION FOR SEQ ID NO: 560

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC

23

2) INFORMATION FOR SEQ ID NO: 561

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40 ACIGTICGGC CRCCCTCACG GAT

23

2) INFORMATION FOR SEQ ID NO: 562

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCI GG IGYIMGIATG

30

2) INFORMATION FOR SEQ ID NO: 563

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT

26

2) INFORMATION FOR SEQ ID NO: 564

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA

29

2) INFORMATION FOR SEQ ID NO: 565

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT

26

2) INFORMATION FOR SEQ ID NO: 566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

5 2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

20 2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35 2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

50 RTIRTIGGIS CIGTIRTIGA TAT

23

2) INFORMATION FOR SEQ ID NO: 570

55 (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT

23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT

23

2) INFORMATION FOR SEQ ID NO: 572

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

35

RTIRTIGGIS CIGTIRTIGA

20

2) INFORMATION FOR SEQ ID NO: 573

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC

20

2) INFORMATION FOR SEQ ID NO: 574

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

343

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG

23

2) INFORMATION FOR SEQ ID NO: 575

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GGTA

25

2) INFORMATION FOR SEQ ID NO: 576

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40

AACTTCRTCA AGAAGGTYGG TTACAA

26

45 2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

55

CATGATTGAA CCATCCACCA

20

60

2) INFORMATION FOR SEQ ID NO: 578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA

20

2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA

20

2) INFORMATION FOR SEQ ID NO: 580

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC

25

2) INFORMATION FOR SEQ ID NO: 581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

5 2) INFORMATION FOR SEQ ID NO: 582

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

20 2) INFORMATION FOR SEQ ID NO: 583

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

35 2) INFORMATION FOR SEQ ID NO: 584

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

50 2) INFORMATION FOR SEQ ID NO: 585

55 (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG

20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA

20

2) INFORMATION FOR SEQ ID NO: 587

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

35

CGTATTATCA AAAGACGAAG

20

2) INFORMATION FOR SEQ ID NO: 588

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAA CTATCGTCCA

20

55

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

347

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40

TCCTGGTTCT ATTACACCAC

20

45 2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

CAAAGCTGAA GTATACGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 593

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACTAACT ATCGCCCACA

20

2) INFORMATION FOR SEQ ID NO: 594

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC

20

2) INFORMATION FOR SEQ ID NO: 595

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

TTAAAGCAGA CGTATACGTT

20

2) INFORMATION FOR SEQ ID NO: 596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

5 2) INFORMATION FOR SEQ ID NO: 597

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

20 2) INFORMATION FOR SEQ ID NO: 598

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

35 2) INFORMATION FOR SEQ ID NO: 599

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

20

50 2) INFORMATION FOR SEQ ID NO: 600

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA

20

2) INFORMATION FOR SEQ ID NO: 601

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

20

GTTTCACGTG ATGATGTACA

20

2) INFORMATION FOR SEQ ID NO: 602

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

35

AAGTTGAAGT TGTGTTATT

20

2) INFORMATION FOR SEQ ID NO: 603

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC

20

2) INFORMATION FOR SEQ ID NO: 604

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT

20

2) INFORMATION FOR SEQ ID NO:605

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT

20

2) INFORMATION FOR SEQ ID NO:606

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40

ATTAGACTAC GCTGAAGCTG

20

2) INFORMATION FOR SEQ ID NO: 607

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 29212

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

60

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACATCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: ATCC 19434

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTCTTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

55

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
15	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCCCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
20	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
25	AAGGTGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae* Rd

(B) STRAIN: KW20

(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	TGAACACATC	TTATTAGGTC	100
50	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAACT	200
	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCCTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
55	TGACCAACCG	TTCCTTCTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAGAAC	GAGGTATTAT	CCGTACAGGT	450
	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAACGTGGT	600
60	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650

	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCACTCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTGGT	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 611

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCACCTAAT	ATCGCCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAACCTG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAA				818

2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

355

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCA	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 778 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTCGCGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTCGATTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 bases

60

356

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*
(B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTTAAGCACT	TGATCGTTTT	100
15	CTTGAACAAA	GTAGATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TAAAGGTTT	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350
20	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
25	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45	CCATTCTAGT	TGTATCTGCA	ACAGATGGAC	CAATGCCACA	AACACGTGAA	50
	CATATTTTAT	TGTCACGTCA	AGTAGGTGTT	AAATATTTGA	TCGTCTTCTT	100
	GAACAAAATC	GACTTAGTAG	ATGATGAAGA	ATTGATTGAT	CTTGTCGAAA	150
	TGGAAGTTTC	TGAATTATTA	AGCGAATATG	GTTTCCCAGG	TGACGATACA	200
50	CCAGTCATCA	AAGGTTCAGC	ATTAAAAGCT	TTACAAGGAG	ATCCTGATGC	250
	AGAAGCAGCT	ATCATGGAAT	TGATGGATAC	TGTTGATGAA	TATATCCCCA	300
	CACCAGAACG	TGATACAGAC	AAACCATTAT	TGTTACCAGT	GGAAGATGTC	350
	TTCTCAATCA	CAGGTCGTGG	GACTGTTGCT	TCAGGTCGTA	TCGATCGTGG	400
	TGCAGTTCGT	GTAGGTGATG	AAATCGAAAT	CGTCGGTATC	AAACCTGAAA	450
55	CACAAAAAGC	TGTTGTAAC	GGGGTCGAAA	TGTTCCGCAA	GACATTAGAC	500
	TATGGTGAAG	CAGGAGATAA	CGTTGGGGTA	TTGTTACGTG	GTATCCAACG	550
	TGAAGATATC	GAACGTGGAC	AAGTAATCGC	AAAACCAGGT	TCAATCACAC	600
	CACATACAAA	ATTCAAAGCA	GAAGTGACG	TATTGACAAA	AGAAGAAGGT	650
	GGACGTCATA	CACCATTCTT	CAATAACTAT	CGTCCACAAT	TCTACTTCCG	700
60	TACAACTGAC	GTAAC TGGA	CAATCGTTTT	ACCTGGAGGC	ACTGAAATGG	750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCAGTT 890
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT	TAGTAGTATC	TGCTACTGAT	GGCCCAATGC	CACAAACACG	50
TGAACATATC	TTGTTATCAC	GTCAAGTAGG	GGTTAAACAC	TTAATCGTCT	100
TCTTGAACAA	AGTTGATTTA	GTTGATGATG	AAGAATTGAT	CGATTTAGTT	150
GAAATGGAAG	TTCGGGAATT	GCTTTCTGAA	TATGGTTTCC	CAGGCGATGA	200
TATTCCAGTA	CTTAAAGGTT	CTGCTTTGAA	AGCTTTAGAA	GGCGATCCTG	250
AACAAGAACA	AGTAATCCTT	GACTTGATGG	ATACGGTTGA	TGAATACATC	300
CCAACGCCTG	AACGTGATAC	TGACAAACCA	TTCTTGTTAC	CAGTCGAAGA	350
TGTCTTCTCA	ATCACAGGAC	GTGGTACGGT	TGCATCTGGT	CGTATCGATC	400
GTGGGGAAGT	TAAAGTCGGT	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
GAAGTGCAAA	AAGCTGTCTG	AACTGGACTA	GAAATGTTCC	GTAAGACATT	500
GGATTACGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
CTCGTGATGA	AATCGAACGT	GGACAAGTAT	TAGCTAAACC	AGGTTCAATC	600
ACTCCACATA	CGAAATTCAG	TGCAGAAGTT	TATGTATTGA	CGAAAGAAGA	650
AGGTGGCCGT	CATACGCCA				669

2) INFORMATION FOR SEQ ID NO: 617

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

CGGGGCAATT	TTAGTTGTAT	CTGCAACTGA	TGGCCCAATG	CCACAAACAC	50
GTGAACACAT	TTTGTTAGCT	CGTCAAGTAG	GGGTAAATA	TTAATCGTC	100
TTCTTGAACA	AAACAGATTT	AGTTGATGAT	GAAGAATTAT	TGGAAC TAGT	150
TGAAATGGAA	GTTCTGTAAT	TATTAAATGA	ATACAATTTT	CCTGGCGATG	200
ATATTCCTGT	TATTCGCGGA	TCTGCTTTAA	AAGCATTAGA	AGGCGATCCA	250
GAACAAGAAG	AAGTAATTAT	GAAC TTGATG	GATACTGTGG	ATGAATATAT	300

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGGGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTT	CGTAAAACCT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

15 2) INFORMATION FOR SEQ ID NO: 618

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAATCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAAACCTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
45	AGGTGGACGT	CATACACCAT	CTT			673

2) INFORMATION FOR SEQ ID NO: 619

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

	TTTCATATTT	TTAAGGATTT	TGTTTTAGCA	CCCATCCGAC	CTCAGTCAAT	50
5	ATATCCTTTC	GCGACCAGGC	TTTCCTCCCT	TTTGCTGCTA	ACTGGTTACA	100
	GATTTTCCTA	TTTTTGGTCA	TTTTTATCTT	TGAAACTGAT	TAAGCTGAAA	150
	AAATTTGAGC	TTCTTTGTTG	TAAACTATTT	TGTGCTTTCA	GTTTTATTCT	200
	AGCTCGACAA	AGGTAACAGA	CAAAAATGTC	AGCTTTATTA	CCAAGATTAC	250
	TCACAAGAAC	AGCTTTTAAA	GCTTCTGGGA	AACTTCTGAG	GCTCTCTTCA	300
10	GTAATTTCTA	GGACCTTTTC	TCAAACACT	ACTTCCTATG	CAGCTGCTTT	350
	TGATCGTTCC	AAACCGCATG	TAAATATAGG	TACGATCGGC	CATGTTGATC	400
	ATGGGAAGAC	AACTTTAACC	GCAGCCATTA	CGAAAACGTT	AGCCGCAAAA	450
	GGTGGTGCCA	ACTTCTTGGA	CTATGCTGCC	ATCGATAAGG	CTCCGGAAGA	500
	AAGAGCTCGT	GGTATTACAA	TTTCTACTGC	ACACGTGGAA	TACGAAACGG	550
15	CCAAGAGACA	TTATTCTCAC	GTCGACTGTC	CAGGCCACGC	TGATTACATC	600
	AAGAATATGA	TTACCGGTGC	TGCTCAAATG	GATGGTGCTA	TCATTGTTGT	650
	AGCTGCTACC	GATGGACAAA	TGCCCCAAAC	TAGAGAACAT	TTACTTTTGG	700
	CCAGACAAGT	TGGTGTCCAA	CATATTGTCT	TTTTTGTTAA	CAAGGTTGAT	750
	ACCATTGATG	ATCCAGAAAT	GTTAGAGTTA	GTCGAAATGG	AAATGAGAGA	800
20	ACTTTTAAAC	GAATATGGGT	TTGACGGTGA	TAATGCTCCA	ATTATCATGG	850
	GTTCTGCCCT	TTGCGCTTTG	GAAGGTCGCC	AACCTGAAAT	TGGGGAGCAG	900
	GCCATCATGA	AACTTTTGGA	TGCAGTGGAT	GAGTATATTC	CTACACCTGA	950
	AAGAGATTTG	AACAAGCCTT	TCTTGATGCC	CGTTGAAGAT	ATCTTCTCTA	1000
	TCTCCGGTAG	AGGTACTGTG	GTCAGTGGTC	GTGTGGAAAG	GGGTAATTTA	1050
25	AAGAAAGGTG	AGGAATTGGA	AATTGTTGGT	CACAACTCCA	CCCCATTGAA	1100
	AACAACAGTT	ACTGGTATTG	AAATGTTTAG	AAAGGAATTG	GACTCTGCTA	1150
	TGGCAGGTGA	CAATGCCGGT	GTTTTACTTA	GAGGTATCAG	GAGAGATCAA	1200
	TTGAAGAGAG	GTATGGTCTT	AGCTAAGCCA	GGTACCGTTA	AAGCCCATAC	1250
	AAAGATTCTA	GCCTCTTTGT	ACATTTTATC	CAAAGAGGAA	GGTGGTAGAC	1300
30	ATTCTGGGTT	TGGTGAAAAC	TACAGACCAC	AAATGTTTAT	AAGAACAGCT	1350
	GATGTTACAG	TTGTGATGAG	ATTTCCTAAG	GAGGTTGAAG	ATCATTTCTAT	1400
	GCAAGTTATG	CCAGGTGACA	ATGTTGAAAT	GGAATGTGAT	TTGATCCATC	1450
	CTACCCCAT	AGAAGTTGGT	CAACGTTTCA	ATATCAGAGA	GGGTGGAAGA	1500
	ACTGTTGGTA	CCGGTCTAAT	CACACGTATT	ATTGAATAGA	CTTATTGATG	1550
35	CAACTGGAGT	ATATTTCTAT	ATATTCTGTT	CATTTCCCCT	CTCATAATAT	1600
	ATACTTGTTT	CGTTAAAATT	TTATACGTGT	AAATAAAGTG	CCATAAATTT	1650
	TTCAGCTTTA	CTTTTGGTAG	AGTCCTGCTA	GCACTAGATT	TTACAATTTT	1700
	ATGTGCACAC	ACC				1713

40

2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| 45 | (A) | LENGTH: 18 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Single |
| | (D) | TOPOLOGY: Linear |

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

ATTGGTGCAT TGCTACGT

55

18

2) INFORMATION FOR SEQ ID NO: 621

(i) SEQUENCE CHARACTERISTICS:

60

360

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

15 TGGTGCAATC TTAGTTGTTT CTGCAACTGA CGGTCCGATG CCTCAAACAC 50
 GTGAACACAT TTTATTGTCA CGCCAAGTTG GTGTAAAATA CCTGATTGTT 100
 TTCTTGAACA AAGTTGATTT AGTCGATGAT GAAGAATTGA TCGATTGGT 150
 AGAAATGGAA GTTCGCGAGT TATTGAGCGA ATATGGTTTC CCAGGCGATG 200
 ACACTCCTGT GATCAAAGGT TCCGCATTAA AAGCATTGCA AGGCGATCCA 250
 GATGCTGAAG CTGCTATTAT GGAATTGATG GATACAGTAG ATGAATATAT 300
 20 CCCAACACCA GAACGTGATA CAGATAAACC ATTACTATTG CCAGTGGAAG 350
 ACGTCTTCTC AATTACAGGT CGAGGAACTG TTGCCTCAGG TCGTATTGAT 400
 CGTGGTGCTG TTCGTGTCGG TGATGAGGTA GAGATCGTAG GGATCAAACC 450
 TGAAACACAA AAAGCAGTTG TAACAGGTGT AGAAATGTTC CGTAAAACGT 500
 TAGATTACGG GGAAGCTGGG GATAACGTAG GCGTGTTGTT ACGGGGGATC 550
 25 CAACGTGACG ATATCGAACG TGGACAAGTA CTTGCTAAAC CAGGTTCCAT 600
 TACTCCACAT ACAAATTCA AAGCAGAAGT GTACGTGTTG ACAAAGAAG 650
 AAGGTGGACG TCATACTCCA TTCTTCAACA ACTATCGTCC ACAGTTCTAC 700
 TTCCGCACAA CTGATGTTAC AGGAACAATC ACATTGCCAG AAGATACAGA 750
 A 751

30

2) INFORMATION FOR SEQ ID NO: 622.

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

50 GTCAAAATGGG ACGAATCCAG ATTCCAAGAA ATTGTCAAGG AAACCTCCAA 50
 CTTTATCAAG AAGGTTGGTT ACAACCCAAA GACTGTTCCA TTCGTCCCAA 100
 TCTCTGGTTG GAACGGTGAC AACATGATTG AAGTACCAC CAACGCTCCA 150
 TGGTACAAGG GTTGGGAAAA GGAAACCAAG GCCGGTGTCG TCAAGGGTAA 200
 GACTTTGTGTTG GAAGCCATTG ACGCCATTGA ACAACCATCT AGACCAACTG 250
 ACAAGCCATT GAGATTGCCA TTGCAAGATG TTTACAAGAT TGGTGGTATT 300
 55 GGTACTGTGC CAGTCGGTAG AGTTGAAACC GGTGTCATCA AGCCAGGTAT 350
 GGTGTTACT TTCGCCCCAG CTGGTGTTAC CACTGAAGTC AAGTCCGTTG 400
 AAATGCATCA CGAACAATTG GAACAAGGTG TTCCAGGTGA CAACGTTGGT 450
 TTCAACGTCA AGAACGTTTC CGTTAAGGAA ATCAGAAGAG GTAACGTCTG 500
 TGGTGACGCT AAGAACGATC CACCAAAGGG TTGCGCTTCT TTCAACGCTA 550
 60 CCGTCATTGT TTTGAACCAT CCAGGTCAA TCTCTGCTGG TTAATCTCCA 600

361

GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCTG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

2) INFORMATION FOR SEQ ID NO: 623

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
25 CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTCAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
30 CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCTTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGCT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGCTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTCACACT	GCCCGTAAGC	CTGACCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTCGATTTCG	CGTCCGAGA				1269

50

2) INFORMATION FOR SEQ ID NO: 624

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 753
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

362

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 36801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTCGTTT	100
10	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
15	TATGGTTGTT	ACTTTCGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAAA	GGGTTGTGAC	TCTTTC AATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
20	CCAGTCTTGG	ATTGTCACCC	TGCCACATT	GCTTGTA AAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	750
	CCA					753

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

	CGTTGAAGAC	ACGACCCAAA	GSTATCC	26
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2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

	TACCACCTTT	TAAGTAAGGT	GCTAAT	26
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2) INFORMATION FOR SEQ ID NO: 627

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

ATTGTCTATA AAAATGGCGA TAAGTC

26

2) INFORMATION FOR SEQ ID NO: 628

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA

26

2) INFORMATION FOR SEQ ID NO: 629

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA

25

2) INFORMATION FOR SEQ ID NO: 630

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA

22

2) INFORMATION FOR SEQ ID NO: 631

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

CAGACCAACY GAIAARCCAT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 632

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

CCCTTTGGTG GRTCSTKCTT GGA

23

2) INFORMATION FOR SEQ ID NO: 633

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 634

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA

26

5

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

20 AAACCRGTIA RRGCRACCTCT IGCTCT

26

2) INFORMATION FOR SEQ ID NO: 636

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 637

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50

ACGTCAGTIG TACGGAARTA GAA

23

55 2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT

26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTTWCACAC CWGTIACA

28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA

40

23

2) INFORMATION FOR SEQ ID NO: 641

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG

26

60

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA

23

2) INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA

23

2) INFORMATION FOR SEQ ID NO: 646

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

15 ATCGACAAGC CITTCTIAT GSC

23

2) INFORMATION FOR SEQ ID NO: 647

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

30

ACGTCCGTSG TRCGGAAGTA GAACTG

26

2) INFORMATION FOR SEQ ID NO: 648

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

45

ACGTCSTSG TRCGGAAGTA GAACTG

26

2) INFORMATION FOR SEQ ID NO: 649

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

5

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

20 TTACGGAACA TYTCAACACC IGT

23

2) INFORMATION FOR SEQ ID NO: 651

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA

25

2) INFORMATION FOR SEQ ID NO: 652

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

50

CCWAYAGTIY KICCCICCYTC YCTIATA

27

55 2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT

20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA

22

60

2) INFORMATION FOR SEQ ID NO: 657

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA

2) INFORMATION FOR SEQ ID NO: 658

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT

2) INFORMATION FOR SEQ ID NO: 659

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTIG TTTWGGTTT RAT

2) INFORMATION FOR SEQ ID NO: 660

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG

2) INFORMATION FOR SEQ ID NO: 661

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661
 15 GTAGAAYTGT GGWCGATART TRT

23

2) INFORMATION FOR SEQ ID NO: 662

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC	CTCGTTGTTG	CTGCCACCGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACGT	TCTGCTCGCT	CGCCAGGTCG	GCGTTCCTTA	CATCCTCGTT	100
	GCTCTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	CGAGATGGAG	ATCCRTGAGC	TGCTCGCTGA	GCAGGATTAC	GACGAAGAGG	200
	CTCCAATCAT	CCACATCTCC	GCACTGAAGG	CTCTTGAGGG	CGACGAGAAG	250
40	TGGACCCAGT	CCATCATCGA	CCTCATGCGA	GCTTGCKATG	ATTCCATCCC	300
	AGACCCAGAG	CGTGAGACCG	ACAAGCCATT	CCTCATGCCT	ATCGAGGACA	350
	TCTTCACCAT	CACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCTCCCTGA	AGGTCAACGA	GGACGTCGAG	ATCATCGGTA	TCCGCGAGAA	450
	KGCTACCACC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGT	AAGCTTCTCG	500
45	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTCCG	TGGCGTTAAG	550
	CGCGAAGACG	TTGAGCGTGG	CCAGGTTGTT	GTTAAGCCAG	GCGCTTACAC	600
	CCCTCACACC	GAGTTCGAGG	GCTCTGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GTGGCCGCCA	CACCCCATTC	TTGACAACCT	ACCGCCACCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTTCCTGAGG	GCACCGAGAT	750
50	GGTCATGCCT	GGCGACAACG	TCGACATGTC	CGTCACCCTG	ATCCAGCCTG	800
	TCGCTATGGA	TGAGGGCCTG	CGCTTCGCTA	TC		832

55 2) INFORMATION FOR SEQ ID NO: 663

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

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10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA      50
   CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA      100
   CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT      150
   ACCTTGGGCC GGATCATCAA CGTTGTCTGGT GAGCCCATCG ACGAGCGTGG      200
15  TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT      250
   TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT      300
   GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG      350
   TGGTGCCGGT GTCGGTAAGA CCGTGTTTCAT CCAGGAGTTG ATTAACAACA      400
   TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT      450
20  ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT      500
   CAACTTGGAG GCGGACTCCA AGGTGGCCTT GGTGTTTCGGT CAGATGAACG      550
   AGCCCCCGGG GGCTCGTGCC CGTGTGCCTT TGACCGGTTT GACCATTGCC      600
   GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA      650
   CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC      700
25  GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT      750
   TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT      800
   GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCCGCCA      850
   CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCTCG TGGTATCTCC      900
   GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGAATCCA AGTCGAGATT      950
30  GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG      1000
   TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT      1050
   TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC      1100
   CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTCGCTGTC GCCGAGGTTT      1150
   TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG              1192
35

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2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

10	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
15	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
20	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCC	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
25	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
30	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTTC	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
	AAGTTCGTTT	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
35	ACCATTGCTG	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCTG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

40

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

	ATGGTTTTGC	CAAGACTATA	TACTGCTACA	TCCCGTGCTG	CTTTTAAAGC	50
	AGCCAAACAA	TCCGCTCCGC	TTCTATCCAC	TTCGTGGAAA	AGATGTATGG	100
	CCTCAGCTGC	TCAATCTACT	CCAATCACCG	GTAAAGTTAC	CGCTGTCATT	150
60	GGTGCCATTG	TTGACGTTCA	TTTTGAACAA	TCAGAGTTGC	CCGCTATTTT	200

	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGT	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCAG	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCT	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCGAAGA	GGTATTTTCAG	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCTG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCT	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

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2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: Y

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCGGGAG	200
	ACACTTGCCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAGGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTG	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTTTG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACTT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGACTCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTCCGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCAGGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCCG	AGA	1293

15

2) INFORMATION FOR SEQ ID NO: 668

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium glutamicum*

(C) ACCESSION NUMBER: X77034

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGCTCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTTCG	TGAACTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTA	TGCCTATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCTG	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTT	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTCGAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTGCGT	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCGT	GTCACCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 669

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

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15  ATGGCTACTG GAAAGATTGT CCAGGTAATC GGCGCCGTAG TTGACGTCTGA      50
    ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA      100
    ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT      150
    ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT      200
    GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAAGCGA      250
20  CTCTGGGCCG TATCATGAAC GTACTGGGTG AACC GGTCGA CATGAAAGGC      300
    GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA      350
    CGAAGAGCTG TCAAACCTCT AGGAACCTGCT GGAAACCGGT ATCAAAGTTA      400
    TCGACCTGAT GTGTCCGTTC GCTAAGGGCG GTAAAGTTGG TCTGTTCCGT      450
    GGTGCGGGTG TAGGTAAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT      500
25  CGCGATCGAG CACTCCGGTT ACTCTGTGTT TCGGGCGTA GGTGAACGTA      550
    CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC      600
    GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG      650
    TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG      700
    AAGGTCGTGA CGTTCGTCTG TTCGTTGACA ACATCTATCG TTACACCCTG      750
30  GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG      800
    TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCGTCAG GAACGTATCA      850
    CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT      900
    GCGGATGACT TGACTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA      950
    CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG      1000
35  CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT      1050
    GGTGAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG      1100
    TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT      1150
    CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC      1200
    CTGTCCCAGC CGTTCCTTCGT GGCAGAAAGTA TTCACCGGTT CTCCGGGTAA      1250
40  ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG      1300
    GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC      1350
    GAAGAAGCTG TGGAAAAAGC CAAAAAATT TAA                          1383
  
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2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: NCTC 11638
 (C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTGAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTGCCT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTCACAG	350
10	AAAAGCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCT	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	CGGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTCA	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

35 2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
 (B) STRAIN: DSM 792
 (C) ACCESSION NUMBER: extracted from AF101055

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTTCA	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AAACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAGTTG	250
	GAGAAAATGT	TTTAGGACGT	CTTTTTAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGGTGG	AAAAATCGGT	450

	TTGTTCCGGTG	GTGCCGGTGT	TGGTAAAACA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CACTTGCAAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTCCCTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTTC	1150
15	ATGAACTTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAAATGA	TGGAAAGCTA	1400
20	A					1401

2) INFORMATION FOR SEQ ID NO: 672

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1509 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 30 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 35 (A) ORGANISM: *Cytophaga lytica*
 - (B) STRAIN: DSM 2039
 - (C) ACCESSION NUMBER: M22535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

40	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCA A CTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

15 2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
 (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTG TTCAGGA	150
	AATCCAATTC	AGGTT CCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAAGTC	GTGAAGGTAA	500
	TGACTTGTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTC	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGGTTCT	ATAACATCT				819

50

2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

	AGAGCGAAGT	ACCAAGTGTT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
	GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
	CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
10	AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
	CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
	CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
	AGTCTAGTGC	AACTGAACTT	TTGGAAACGG	GTGTAAAGGT	TATCGACCTG	350
	ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTCG	GTGGTGCGGG	400
15	TGTAGGTAAG	ACCGTTAACA	TGATGGAACT	TATCAACAAC	ATCGCGCTAC	450
	AGCACTCAGG	TTTGTCAGTA	TTTGCTGGGG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
	ACAACCAGAA	CTGTGCAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
	CACCAGGCAA	CCGTCTGCGT	GTAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
20	AAGTTCCGTG	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
	CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
	CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
	CAAGAACGTA	TCACGTCAAC	CAAAAAGGT	TCTATCACCT		840

25

2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

	CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100
45	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTCGTGAGC	TGCTGTCTGA	GTACGATTTT	CCAGGTGATG	200
	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
	TCCAGAGCCA	GAGCGTGCAG	TAGACATGGC	ATTCTTGATG	CCAATCGAAG	350
50	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACRRTACG	TGGTACTAAG	550
	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
55	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
60	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

2) INFORMATION FOR SEQ ID NO: 676

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania enriettii*
 15 (B) STRAIN: ATCC 50120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

20	CTTCTCGGAT	GGCGTGCCGC	CGGTGCTGAC	GGCGCTGGAC	GTGACGGAGG	50
	AACCTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
25	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTCCGC	GGCGTTGGGG	500
	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
30	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
	GACAAATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
	GGGCCGTCATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
35	TCGGCATGTT	GCAGGAGCGC	ATCACGTGCA	CGACGAAGGG	GTCGATCACG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCCGCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCCGCGGTCA	ACCCACTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
40	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
45	AGTCGTTCTC	CGGTTTGCTG	ATGGGGTTCG	ACGACCAGAT	TCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 677

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia microtti*
 60 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGGTAT	TACTATTGAC	ATTACTCTCT	50
5	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTC	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCACACAT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

2) INFORMATION FOR SEQ ID NO: 678

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGCCCTG	ACTAAAACTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTAATTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCCGATT	CACCCAGGCC	GGTTCGAGG	TGTCTGCCCT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

60 2) INFORMATION FOR SEQ ID NO: 679

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

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TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT      50
ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG      100
TACCACGAAA TGAGGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA      150
GGTCGCTCTT GGTGAGTTCT TTTTTTTGGG AGCTAATTAG TCGATGACGT      200
GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC      250
CCCTGGAGCC CGTGCCCGAG TAGCTCTTAC TGGTTTGACC ATTGCCGAGT      300
ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT      350
TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT      400
CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA      450
TGCAAGAGCG AATGTAAGTT GCATTTTTTG TGATTTTACG GCAAGTCTTG      500
ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG      550
TC

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2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

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TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC      50
GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT      100
ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTLAGAT GATCATAAAT      150
AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT      200
AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT      250
TTTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC      300
CTTTTTTATA AAATTAATCA GGTCTTGTCG GTGGTCAAAA GGTGTTGATG      350
ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT      400
CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA      450
AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT      500
CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCTG ATTTATTAGC      550
TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCCGGTGGT GCTGGTGTAG      600
GTAAACTGT CTTGATTCAA GAACTTATTA ACAACATTGC TAAAGCCCAT      650
GGTGGTTACT CTATTTTCTG TGGTGTGGT GAACGTACTC GTGAAGGTAA      700

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CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
CGTGCCCGTG	TTGCTTTAAC	TGGTTTAAAC	ATTGCTGAAT	ACTTCCGTGA	850
TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5 CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
TATTACTACT	ACCAAGAA				1018

10

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

25

2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

40

2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

55 GTIACIGGIT CISWIAWRTC ICCICC

26

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2) INFORMATION FOR SEQ ID NO: 684

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
30	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTGA	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTC	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAAAGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCAGTGTTC	CTGCTGATCA	TAAACTTATC	TTGAAAATA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTTACTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAACTCA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTCA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTTAC	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCTTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTCT	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTTC	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTC	TGGGGGTTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAATA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTGGAG	ATTTATTAAC	CACTATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

2) INFORMATION FOR SEQ ID NO: 685

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Enterococcus hirae*
- (B) STRAIN: ATCC 9790
- (C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

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	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTTG	GTACGTGGAT	GAAACGAAGA	TCATTTCAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
	AGCTGACGAT	GATGCAAAA	TGGCCAGTAC	GTCGTGGTCC	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
55	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCCGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTT	CTGAACTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGGA	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAACCTG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCTT	GAAGTAGCAA	AATCGATTCT	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

20 2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029
 (C) ACCESSION NUMBER: Genome project

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCA	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTGCA	GGAGCTCTTG	TTACGTTTTT	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTT	250
	TCGATGGACT	TCAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	TGTGCTGTC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTTCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTGCT	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCTAGA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCAGTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTGT	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTTC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

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2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Halobacterium salinarum*
 (C) ACCESSION NUMBER: S56356

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTGC	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
	CCAGCCCGTC	GACAACACGG	GCGAACCGCT	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TCGACGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGGCCGT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCGGTTG	CCGGGCGTGA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCGGCG	AGGAGGGGTA	TCCGCGGTAC	CTGGCCGCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTCAC	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTCGACA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

CCGAGGACCA	GCAGCTCAGC	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1500
TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCCCCCGA	1550
GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5 GCGCGGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGACG	ACGAGCACGA	1700
GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
TCTACTGA					1758

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2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 3118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
 (C) ACCESSION NUMBER: L09234

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
30 AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
GAACTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
35 TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
AGTGGGACTT	CAGTCCCGTC	AGTGTCGAAG	TTGGAAGCCA	CATTACTGGT	500
GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
GCTGCTGCCG	CCCCGTGCCA	AGGGAAC TGT	CACGTACATT	GCAGAACCTG	600
GAAACTACAC	AGTTGATGAT	GTTGTCCTGG	AGACAGAATT	TGACGGCGAG	650
40 CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCAGGCC	700
TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
CTCAAAC TCC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
45 AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCGTT	GGAGATTGAT	950
GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000
AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
50 TGAAATGCCT	CGCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAG	1250
AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGAGAG	1300
CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
55 TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
CAAGAATTTT	CCAGAGTTTG	TCCCCTGCG	TACAAAGGTG	AAGGAGATTT	1500
TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
GGATGATTTC	CTGCAACAGA	ACAGCTATTC	ACCATATGAC	CGTTTCTGCC	1650
60 CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700

	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAA S ATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTGAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCAG	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCGG	TACAGAGGCA	ATAATCTGAT	AACCTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTG TG	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAACCTCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCCTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTCAT	TAGCATTTCA	CTGTTGTCAC	3100
	ATAAATTATG	CCCGGAAT				3118
30						

2) INFORMATION FOR SEQ ID NO: 689

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1836 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Plasmodium falciparum*
 - (B) STRAIN: 3D7
 - (C) ACCESSION NUMBER: L08200
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAAC	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTCTGTA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCTG	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTTGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTAGCT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCTATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACCTAC	1250
15	AGCAACCATG	TCTATTGTTT	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCC	ATTACAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

30 2) INFORMATION FOR SEQ ID NO: 690

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3216 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: X2180-1A
 (C) ACCESSION NUMBER: J05409

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCTGTGTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCTGGGT	300
	CTGATGGAAG	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTCGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGAATTG	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTC	ACTCTTTACC	ATACTTGGCC	650
60	TGTTTCGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTGCAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTGG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAAGTGT	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGGTAA	TGGTATTCGC	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTC	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCTCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGTCTG	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACTTATGAT	GCTTTCTGTC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1860 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGTA	CGAACTCGTT	150
15	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTTAA	AGCAAATTTT	350
	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
20	TTAATCGTGA	GCATAAGTGG	GATTTCACAC	CAAATAAGGA	TTTACGCATT	450
	GGCGATCATG	TATCCGGTGG	TGATGTTTTT	GGTTCTGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
25	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCACAATCT	CTTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCG	850
	GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
30	GAAC TAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
	TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
35	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTCTCTG	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTGG	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
40	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
	GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
45	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
	TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
	GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
	GACTGAGTAA					1860

50

2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

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10  ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
    GAAGGCCGTC TCCGGGCCAG TTGTCAATTGC TGAAAACATG GGCGGTAGCG      100
    CTATGTATGA GCTTGTGCAG GTAGGTTCTT TCCGGTTAGT GGGCGAGATC      150
    ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
    TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTCGC      250
15  TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
    CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG      350
    CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTTAAGCCAT      400
    GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
    GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT      500
20  GCGGGGCCGT GTTACTTCCA TTGTTCTTTC AGGAAATTAC ACCCTCCAAG      550
    ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAAATT      600
    ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
    CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
    CATCCGTCCA GGGTGGAAACA TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
25  AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT      800
    TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
    TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
    ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC      950
    TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG      1000
30  ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT      1050
    GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG      1100
    TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG      1150
    CGGGGCGCGT GACATGCATC GGTGGGCCAA AACGCGAGGG CTCAGTAACC      1200
    ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC      1250
35  GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC      1300
    TTGCGCAACG TAAACACTTT CTTCTGTGTA ATTGGCTCAT TTCCTATTCA      1350
    AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA      1400
    CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CTTTCAGCGT GAGGAAGAGT      1450
    TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC      1500
40  AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA      1550
    GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT      1600
    GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA      1650
    GCTGAGTCCG CTGGGGAAC TAAGATTACG TGGAAGTACA TTCGTGAAAT      1700
    GATTCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC      1750
45  AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA      1800
    ATTGTCAGCG CATTCGCCTC GCTGCTGCAA TAA                      1833
  
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50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
 (B) STRAIN: HB8
 (C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

	ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCGGCGG	TGATCGCCAA	50
	GGGCATGCTC	GGGGCCCGCA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
	GCCTCGTGGG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	CTTCGTCCAG	150
10	GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
	GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCC	CGGGATGCTG	AACGGCATCT	250
	ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
	TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
	GGCCTGGACG	CCCATGGTCA	AGCCCCGGGA	CGAGGTGCGG	GGGGGTATGG	400
15	TCCTGGGCAC	GGTGCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
	CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCGCCG	GGGAGTACAC	500
	CGTGGAGGAG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
	ACCACACCTG	GCCCGTTCGC	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
	CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGGACG	TCCTCTTCCC	650
20	CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
	AGACCGTGAC	CCAGCAGTCC	CTGGCCAAGT	GGTCCAACGC	CGACGTGGTG	750
	GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
	GGAGTTCCCC	GAGCTCACCG	ACCCCAAGAC	GGGTGGGCC	TTGATGCACC	850
	GCACCGTCTT	CATCGCCAAC	ACCTCCAACA	TGCCCGTGCG	CGCCCGCGAG	900
25	GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
	CTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
	TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCGCCGA	GGAGGGCTAC	1050
	CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCC	TTCTACGAGC	GGGCGGGCAA	1100
	GGTCATCACC	CTGGGCGGCG	AGGAGGGGGC	GGTGACCATC	GTGGGGGGCCG	1150
30	TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
	AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
	CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCEG	1300
	CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
	CGCGACGCCA	TCTCCGAGCT	TTTGCAGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
35	CGTCCAGCTC	GTGGGGCCGG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
	TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
	CACGAGGTGG	ACGCCTACTG	ATCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
	GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
	TTTCCATAGA	CGAGATCCTG	CAGCTCCCCG	TTCTGGAGCG	CATCGGCCGC	1650
40	GCCCCGTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
	GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
	CCTTCTGA					1758

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTTGTG C

60

21

2) INFORMATION FOR SEQ ID NO: 695

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

GTTTCACGTG ATGACGTACA

20

2) INFORMATION FOR SEQ ID NO: 696

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

ATIGGICAYR TIGAYCAYGG IAARAC

26

2) INFORMATION FOR SEQ ID NO: 697

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

CCIACIGTIC KICCRCCYTC RCG

23

2) INFORMATION FOR SEQ ID NO: 698

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

398

(A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

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5  GTGTCTAAAG AAAAATTGTA ACGTACAAAA CCGCACGTTA ACGTTGGTAC      50
   TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA      100
   CCGTACTGGC TAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC      150
   GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTTCTCA      200
10  CGTTGAATAC GACACCCCGA CCCGTCACTA CGCACACGTA GACTGCCCCG      250
   GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC      300
   GGC GCGATCC TGGTAGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG      350
   TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      400
   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGGT      450
15  GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGCGGACGA      500
   CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG      550
   AGTGGGAAGC GAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT      600
   CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      650
   CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC      700
20  GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      750
   ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      800
   CGAAGCCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      850
   GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG      900
   CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG      950
25  CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     1000
   GTACTACTGA CGT GACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG     1050
   GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT     1100
   CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG     1150
   TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA                      1185
30

```

2) INFORMATION FOR SEQ ID NO: 699

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35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

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40  (ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

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45  GTIACIGGYT CYTYRARRTT ICCICC                                     26

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2) INFORMATION FOR SEQ ID NO: 700

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50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
55  (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

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60

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5 2) INFORMATION FOR SEQ ID NO: 701

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

20 2) INFORMATION FOR SEQ ID NO: 702

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

35 2) INFORMATION FOR SEQ ID NO: 703

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

50

2) INFORMATION FOR SEQ ID NO: 704

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG

20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA

20

2) INFORMATION FOR SEQ ID NO: 706

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

35

TGAAATCTTC ACATCCAACA

20

2) INFORMATION FOR SEQ ID NO: 707

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GTAA

25

2) INFORMATION FOR SEQ ID NO: 708

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

60

401

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATIAAT

26

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1656 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Borrelia burgdorferi*
(C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
30	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAAGATA	AAAAGTGGAA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
	AATTGAGGGA	ACTG TTCACC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACCTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTTCCTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
45	AATGGACAGG	ACTTG TATTA	TTTGTAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTC TTAA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	GTGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTTAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGCTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAAATT	CATTTGATTC	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAAACT	1500
	AACTTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650
 ATTTAG 1656

5

2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: extracted from AE000520

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC 50
 CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCTG 100
 25 ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC 150
 AAGGCGGTCTG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA 200
 GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT 250
 TAATCGGCAC CATTATGAC GGTATTGAGC GCCCACTTGA GCGCCTCTTC 300
 CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTCAC AACCGCTTGA 350
 30 TGGCTCCGTA CGCTGGGATT TTCGTCTCTCA TTGTAACGAG CGCGGTGAGG 400
 CCCTGTGCGC GGGGATTCCG ATTGCACCTG GTTCAGTGTT AGGGACCGTG 450
 CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG 500
 GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG 550
 AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTCTT ATCCCAGTAC 600
 35 TGGCCAGTGC GTCGTGCGCG TCCTTTCAGC AAAAACTTG CAGTGTGTGA 650
 GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTTTCTTC CCCCTATCAA 700
 AGGGAGGAAC GCGGCTATT CCAGGGGAT TTGGAAGTGG GAAGACAATG 750
 ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGTACAT 800
 CGGCTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTC 850
 40 CCAAATCAT CGATCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT 900
 TTGATCGCAA ATACGTCCAA TATGCCTGTG TCCGCACGCG AGGTGTCGCT 950
 GTATTGAGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG 1000
 TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA 1050
 TTGTCTGGGC GCATGGAAGA AATGCCTGCG GAGGAGGGAT TCCCTGCGTA 1100
 45 CCTTCCGACG CGTCTTGAGC AATTTTATGA GCGCGCAGGA CGCGTGGAAA 1150
 CCTGTGTGGC GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTTCTCCC 1200
 CTGGGTGGAG ATTTCTCTGA GCCGGTGACG CAGCACACAA AGCGCTTCAT 1250
 CCGTTGCTTT TGGGCCTTGG ATCGTGAAGT TGCACACGCG CGTCATTACC 1300
 CTGCCATTGG GTGGATAGAT TCATACTCTG AATATGCGCA GGAAGTAAGT 1350
 50 GCATGGTGGA GTAAGTATGA CCCGCGCGCA GGCGCGTTGC GCGCCGACGC 1400
 CTTGGATTGG CTGAGAAAGG AACAGCGGTT ACAGCAAATT GTCAGGCTTG 1450
 TCGGTCTCTG TCGCTGCCTT GGAGAAGATC GTCTGGTGCT AATGGTGTGT 1500
 GAAATGATCA AAGGTGGCTT TCTGCAGCAG AACGCTTTTG ATCCGACGGA 1550
 TGTGTTCTCC TGTCCGAAA AGCAGGTGCA GATCTTGCGT ACCATAGTGG 1600
 55 ATTTTCACGA ACGTGCCGTG GTGCTGCTGC GTGCAGGTAT TTCGCTTTCT 1650
 GCGCTGTCCC AGCTTTCGTG CCGGGAGCTC ATCGTACGTA TGAAAACCTAC 1700
 GTACGGGAAT GAGGATGTAC ACAAGATGCA GAAAGTGTAC GACACGATGT 1750
 GCACTGAGTT TGACCAACTG AGTGTGTGTG CTGCCGCGCG CACACAAGGG 1800
 GGGGAGAAAG TCGAATGA 1818

60

2) INFORMATION FOR SEQ ID NO: 711

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: MoPn

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
20	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTGAGG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACTTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
25	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTT	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTGTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
30	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTTAGAA	600
	GGGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
35	TGTAGAAATT	CTTCAGGAGT	TCCCGCATT	GACAGATCCT	CATACGGGGC	850
	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTTCAG	GGCGATTAGA	AGAAATCCCT	1050
40	GGAGAAGAAG	CTTTCCCAGC	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTA	1100
	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGAGCAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
45	CTAAGTACTT	GGATTCTGTG	GCGGAGATTT	TAGAGAAAAA	AGTTCCAGGA	1350
	TGGGGAGATT	CCGTAAATAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400
	AATTGGTAAG	CGAATAGAAG	TTGTTGGGGA	AGAAGGGATT	TCTATGGAAG	1450
	ATATAGAAAT	CTTTTTGAAA	TCAGAGTTGT	ATGATTTCTG	TTACTTACAG	1500
	CAAAACGCTT	TCGATGCAGA	GGACTGTTAT	TGTCCTTTTG	ATCGTCAAAT	1550
50	AGAGCTTTTT	TCTTTAATGA	GTCATATTTT	TAGCTCTAGA	TTCTGTTTTG	1600
	ATTGTCCAGA	TAATGCTCGG	AGTTTCTTTT	TAGAGCTTCA	AAGTAAATTT	1650
	AAAACGCTGA	ATGGTCAAAA	ATTCTTTTCT	GAAGACTATC	AGAAGGGGCT	1700
	AGAAGTGATC	TATAAACTAT	TAGAAAGCAA	AATGGTGTCAG	ACGGCGTAGG	1750
55	TATGCAACA	ATATATACAA	GAATTACGG			1779

2) INFORMATION FOR SEQ ID NO: 712

60 (i) SEQUENCE CHARACTERISTICS:

404

(A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTtagCTGA	50
15	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTCGC	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTCAAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GCCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATACAT	TTCAAGAAGT	AACCCACAGT	300
20	AACTTTTTAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCTTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAAG	CAGGTGACTT	500
	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
25	GTTTTAGCAT	GATGCAAAAA	TGGCCCGTTC	GGCGGGGACG	TCCCATTTTA	600
	GAAAAACTAA	GTCCCAAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTTC	CCAATTACGA	AAGGCGGAGC	GGCAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTTCAGCAC	AAATTGCTAA	GTGGGCCGAT	750
	GTCGACTTAG	TCGTTTACGT	TGGTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
30	AGATGTTTTTA	AATGAATTC	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCGA	ATACGTCAAA	TATGCCGGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965

35

2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: extracted from J04836

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
55	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
60	GGATTTCAAA	CCCATTTGTC	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400

405

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTCTGA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAACCTCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTACTGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCCT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTT	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTTCTG	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

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2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
- (C) ACCESSION NUMBER: extracted from U67477

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTACTGGAGC	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAACTGT	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTTA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAAGAG	AAACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCG	G TTCAGGAAA	AACGGT TACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCCAC	850
	ACTTAGAAGA	TATTAGA AACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTGCT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTA CTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: W83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGC AAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCTG	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGACAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCCT	TCAAACTGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAAGGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950

	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTTCGGTA	ACGTTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
5	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354

2) INFORMATION FOR SEQ ID NO: 716

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGACTCAA	GGGAAGATTA	TAAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
30	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
	GGGTTAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
35	TGATTTTCTA	GTTCGTGGGG	TAGAAGTTCC	AAGTTTGGAT	AGAGATATTA	350
	AGTGGCATT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAAGTGTCAA	GGAAACCGAG	GTAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
40	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	CTTTCAGTA	ACCAAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
45	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
	CAATCAATTA	TGCAACGGAC	AGTTCTGATT	GCTAATACTT	CAAATATGCC	900
	TGTTGCTGCT	CGTGAGGCTT	CAATTTATAC	AGGAATTACC	ATGGCTGAGT	950
	ATTTTCGTGA	TATGGGCTAC	TCTGTGCGCA	TTATGGCTGA	TTCAACTTCA	1000
	CGTTGGGCAG	AAGCGCTACG	TGAAATGTCA	GGACGTCTAG	AAGAAATGCC	1050
50	TGGTGATGAG	GGTTATCCTG	CTTATCTGGG	AAGTCGTATC	GCTGAATATT	1100
	ATGAAAGAGC	AGGACGTTCT	CAGGTTCTAG	GGCTTCCAGA	ACGTGAAGGA	1150
	ACGATTACTG	CTATTGGAGC	TGTATCGCCA	CCTGGTGGAG	ATATTTTACA	1200
	ACCACTTACT	CAAAACACTT	TACGGATTGT	GAAAGTTTTT	TGGGGGCTTG	1250
	ATGCTCCGTT	GGCACAGCGA	CGTCATTTTC	CTGCAATTAA	CTGGCTTACA	1300
55	TCTTATTCAC	TATATAAAGA	CAGTGTGGGC	ACTTATATAG	ATGGTAAAGA	1350
	GAAGACAGAT	TGGAATAGTA	AAATAACTCG	TGCGATGAAC	TACTTACAAC	1400
	GGGAATCTAG	TTTAGAGGAA	ATTGTTTCGTC	TTGTTGGAAT	TGATTCTCTG	1450
	TCTGATAATG	AACGACTAAC	GATGGAAATT	GCTAAACAAA	TTCGAGAAGA	1500
	TTATTTGCAA	CAGAACGCTT	TTGATTCGGT	AGATACATTC	ACTTCGTTTG	1550
60	CAAAACAAGA	AGCAATGCTA	AGTAATATTC	TCACTTTTCG	TGATCAGGCA	1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTAT		1788

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2) INFORMATION FOR SEQ ID NO: 717

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
CACATCCTGC	TGGCGCGTCA	GGTCGGTGTG	CCGTACATCA	TCGTGTTCTT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TCGAAGTACG	ACTTCCCGGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGGCGAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
TCCCAGCGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCTGAT	GCCGGTGGA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCGA	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCGCC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	GCTGCCGAAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTCGATCA	CGGTGAAGCT	GATCGCGCCG	800
ATCGCGATGG	AAGAAGGTCT	GCG			823

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2) INFORMATION FOR SEQ ID NO: 718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
- (B) STRAIN: 1026B

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

60	GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
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	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATGCTGTTCC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGG	350
	AGACGTGTTT	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTC	TGGCGAAGCC	GGGTTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCCG	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

20 2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAGAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGA	TCGAAATGTT	CAGAAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAAGT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACAA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

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2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAAGTATG	CGACCTTGTT	150
GAAATGGAAG	TACGTGAGCT	GTTAAGCGAG	TACGGATTCG	ACGGAGATAA	200
CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
AATACGTTGG	CGCTATCAAA	GAAGTATGAT	ATGCAGTTGA	TGAATTCATC	300
CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCCTGATGT	CTGTAGAAGA	350
CGTTATGACA	ATCACAGGAC	GTGGTACAGT	TGCTACAGGA	CGTGTTGAGC	400
GTGGGGTAGT	AAAAGTGGGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
ACTCAGAAAA	CTGTTGTTAC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
TGGACGTCAC	ACTCCATTCT	TTTCTAACTA	CCGTCCTCAG	TTCTACTTCC	700
GTACAAGTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
GAGAATTATT	AAGCGAATAC	GGATTGACG	GAGACGAATG	TCCAGTAGTA	200
GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
AGACTTAAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
TCACAGGAGT	AGAAATGTTC	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
AGGTCAAGTA	CTAGCAAAAC	CAGGTTTCAGT	AACACCTCAC	AAAAAATTTCG	600
TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAC	700

AGGATCAATC	GCTTTACCAG	AAGGAGTAGA	AATGGTAATG	CCAGGAGACC	750
ATATAGACAT	GAACGTAGAA	TTAATCACAC	CAGTAGCAA		789

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2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
(B) STRAIN: ATCC 12464

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

G TTCAGCAGC	AGACGGTCCA	ATGCCACAAA	CAAGAGAACA	TATACTACTA	50
GCATCAAGAG	TTGGTGTTGA	CTATATCGTA	GTATTCTTAA	ACAAGGCAGA	100
TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTAGAAATG	GAAAGTTAGAG	150
25 AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATCAAG	200
GGATCAGCTT	TAGTAGCATT	AGAAAACCCA	ACAGATGAAA	AATCAATCGC	250
TCCAATCTTA	GAATTAATGG	AAGCAGTAGA	TAGCTACATT	CCAACACCAG	300
AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTTCACA	350
ATAACTGGTA	GAGGAACAGT	TGCAACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
30 TCATGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GAAAGCAGAA	450
AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCA	500
CAAGCTGGAG	ATAATGTTGG	AGTACTTTTA	AGAGGTGTTT	AAAGAACAGA	550
TATCGAAAGA	GGTCAAGTAT	TAGCAAAGAC	TGGATCAGTT	AAGCCACACA	600
GCAAGTTCGT	AGGTCAAGTA	TACGTACTTA	AGAAAGAAGA	AGGTGGAAGA	650
35 CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
AGACGTTACT	GGATCAATCA	AATTACCAGA	CGGAATGGAA	ATGGTTATGC	750
CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCAA	798

40

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 799 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
(B) STRAIN: ATCC 14573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

G TTCAGCAGC	AGATGGTCCA	ATGCCTCAAA	CAAGAGAACA	CATACTACTA	50
GCTTCAAGAG	TTGGTGTTGA	CTACATAGTT	GTTTTCTTAA	ACAAGGCAGA	100
TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTTGAAATG	GAAGTAAGAG	150
60 AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATAAAG	200

	GGTTCAGCTT	TACAAGCATT	AGAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACCTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCCACA	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAAGCTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAAC	700
	AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

15

2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
 (B) STRAIN: ATCC 19406

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCAGAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATTA	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

50

2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTC	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCAGTTCGT	GATACTGACA	AACCATTCAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTGCAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

2) INFORMATION FOR SEQ ID NO: 726

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Enterococcus sulfureus*
 (B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACCTCGTG	ACACTGACAA	ACCATTCATG	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GTAGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GGCGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*
(B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	150
ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	300
ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma pirum*
(B) STRAIN: ATCC 25960D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCCCTAAAA	TGGTTGTTTT	100
CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
CTGAAGAAGT	AAAAGACTTA	TTAAAATCTT	ATGGTTTTGA	TGGTGACAAT	200
ACTCCAATTA	TTCGTGGTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
ATGAGAAGAA	AAAATTAAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
CATTTAAATC	TGTTGTAACA	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
GGTCGTCATA	CTGCTTTCTT	AAACGGTTAT	CGTCCTCAAT	TCTATTTTCAG	700
AACAACCTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
GCTTGTAATA	AGGAAGTAAG	TTT			823

2) INFORMATION FOR SEQ ID NO: 729

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycoplasma salivarium*
 15 (B) STRAIN: ATCC 23064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

	GGAGCAATCT	TAGTTGTTGC	TGCAACTGAT	GGTGCGATGC	CTCAAACCTCG	50
20	TGAACACGTT	TTACTTGCAA	AACAAGTTGG	TGTTCCCTAAA	ATCGTTGTTT	100
	TCTTAAACAA	AATCGATATG	TTCAAGCCAG	AAGAAAGAGC	CGAAATGGTT	150
	GAAATGGTTG	AAATGGACAT	TCGTGACTTA	TTAAACAAAT	ACGACTTTGA	200
	TGGTGACAAT	ACTCCTATTA	TTGCTGGTTC	AGCATTAATA	GCATTACAAG	250
	GTGATCCAGA	ATATGAAAAG	AATATTCTAG	AACTTATGGA	TGCAGTAGAC	300
25	ACATACATTG	ATGAACCTAC	TCGTGATAAA	GATAAACCAT	TCTTAATGGC	350
	TGTAGAAGAC	GTATTTACAA	TTACTGGTCG	TGGAACGTGT	GCTACTGGTA	400
	GAGTAGAACG	TGGTACATTA	CATCTAAATG	ATGAAGTTGA	AATCGTTGGT	450
	CTACGTCCAA	CAATTAAAAC	TGTTGTTACT	GGAATTGAAA	TGTTCCGTAA	500
	AAATTTAAAA	GAAGCTCAAG	CTGGAGATAA	TGCAGGACTT	TTACTACGTG	550
30	GAATTGATAG	AGATCAAGTA	GAACGTGGAC	AAGTTTTGGC	CAAACCAAAA	600
	AGTATTATTC	CTCACACAGA	ATTTGAAGCT	GCTGTGTATG	TTCTAAAAGC	650
	TGAAGAAGGT	GGACGTCACA	CTCCATTCTT	TGAACACTAT	AAACCACAAT	700
	TTTACTTTTCG	TACAACCGAC	GTTACTGGTG	GAATTAAATT	CAAACCTGGA	750
	CGTGAAATGG	TTATGCCTGG	CGAAAATGTT	GAATTTACAG	TTACTTTAAT	800
35	TGCTCCTATT	GCAGTTGAAG	AAGGAA			826

2) INFORMATION FOR SEQ ID NO: 730

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

55	TGGTATGTTT	CGCAGCYGAY	GGYCCATATG	CTCAAACCTCG	CGAACACATC	50
	CTGYTGGCTC	GCCAAGTAGG	YGTACCTTAC	ATCATCGTRT	TCATGAACAA	100
	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGT	GAAATGGAAA	150
	TCCGYGACCT	GYTGTTCMAG	TACGACTTCC	CMGGCGACGA	CTGCCCCAATC	200
	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGYGAYGCTG	GTTACGAAGA	250
60	GAAAATCTTC	GAAYTGGCTG	CTGCTTTGGA	CAGCTACATC	CCAACCTCCTG	300

	AGCGTGCTGT	GGACAAACCK	TTCYTGTYGC	CTATCGAAGA	CGTRTTCTCT	350
	ATCTCTGGYC	GYGGTACMGT	AGTAACYGGY	CGTGTAGAGC	GCGGTRTCAT	400
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450
	CCACTTGATC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCGT	GGTACCAARC	GTGAAGACGT	550
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600
	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCYAACTA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800
	AAGGTCTGCG					810

15 2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
35	GTTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	AACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAGCC	GTTCTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GAATCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
45	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
	CGACGGTCTG	CGT				813

50

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

417

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
(B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
10	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
	GTTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
15	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GA CT CAGAAG	450
	TCTACCTGTA	CTGGCCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
20	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GCGGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
25	CGACGGTCTG	CG				812

2) INFORMATION FOR SEQ ID NO: 733

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

45	TGGTTGTTGC	TGCGACTGAC	GGYCCGATGC	CGCAGACCCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTGAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGYGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
50	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATT	CCGGAACCCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	450
55	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCTAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
60	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750

CGGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 806
 GACGGTCTGC GTTT 814

5

2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
 35 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGAATGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCA 828

40

2) INFORMATION FOR SEQ ID NO: 735

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG 50
 60 TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAACCTGGTA	150,
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAACCTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGGTAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCTGA	TTCACCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
	CTCCAGAGAG	AGATACAGAT	AAACCATTCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
45	CAAGCACAAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAAT	TCTATTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

10	GTCAACATGA	TGGAGCTCAT	CAACAACATC	GCGAAGGAGC	ACGGCGGTTA	50
	CTCCGTGTTT	GCGGGCGTGG	GCGAGCGTAC	CCGTGAAGGG	AACGACTTCT	100
	ACCACGAAAT	GAAGGACTCG	AACGTTCTCG	ACAAGGTCGC	GCTGGTGTAC	150
	GGCCAGATGA	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTGG	CGCTGACGGG	200
	CCTCACGATG	GCCGAGCACT	TCCGTGACGA	AGGCCTCGAC	GTGCTGTTCT	250
15	TCGTCGACAA	CATCTACCGT	TTCACGCTGG	CCGGTACCGA	AGTGTCGGCG	300
	CTGCTCGGCC	GTATGCCGTC	GGCAGTGGGC	TATCAGCCGA	CGCTGGCTGA	350
	AGAAATGGGC	AAGCTGCAAG	AGCGCATCAC	GTCGACGAAG	AAGGGCTCGA	400
	TCACGTCGGT	T				411

20

2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
(B) STRAIN: ATCC 638

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

	TACAAGAGCT	TATTAACAAT	ATAGCTACTC	AACACGGTGG	TATATCAGTA	50
	TTGCGAGGTG	TTGGAGAGAG	AACAAGAGAA	GGTAACGACT	TATTCCATGA	100
40	GATGAGCGAT	ACAGGAGTTA	TAAATAAAAC	AGCTCTAGTA	TTCGGACAAA	150
	TGAATGAGCC	ACCTGGAGCA	AGAATGAGAG	TTGCTTTAAC	TGGTCTTACA	200
	ATGGCTGAAT	ACTTCAGAGA	TCAACAAGGG	CAAGACGTTT	TATTATTCGT	250
	AGATAATATA	TTCCGTTTCA	CTCAAGCAGG	ATCTGAGGTT	TCTGCACTTC	300
	TTGGACGTAC	TCCATCAGCA	GTTGGATACC	AACCAACATT	AGCAACAGAG	350
45	ATGGGTAGAT	TACAAGAGAG	AATAACATCT	ACAAATAAAG	GGTC	394

2) INFORMATION FOR SEQ ID NO: 739

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

	TTAATAAACA	ACATAGCTAA	ACAACATGGT	GGTTTATCAG	TATTTACTGG	50
	AGTTGGTGAA	AGATCAAGAG	AAGGTAATGA	CTTATATCAT	GAAATGAGAG	100
	AGTCAGGAGT	TATTGATAAG	ACAGCATTAG	TATTTGGACA	AATGAATGAG	150
10	CCACCGGGTG	CCAGAATGAG	AGTTGCATTA	ACAGGTCTTA	CTATGGCAGA	200
	GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
	TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
	CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
15	TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

	TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
35	GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
	GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
	CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
	CATTTTAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
	ATTCCGTTTC	ACACAAGCTG	GTTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
40	TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium ramosum*
 (B) STRAIN: ATCC 25582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

60

	TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
	AGTTTTTGGCT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
	ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
	CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
5	TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
	TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
	TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
	CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

10

2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12964

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
30	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAACTA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTGG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
35	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

2) INFORMATION FOR SEQ ID NO: 743

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTAGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
60	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGA~~G~~CACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

5

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

TTCCCCCGCA CGCATGCCCA AGGTGTTCTGA TGCCCTGAAG CTCGACGGCT 50
CGGCCCTGAC GCTTGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
ACCATCGCCC TGGGTTCGTC CGACGGTCTG CGTCGCGGCC TGATGGTGTC 150
25 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
GTCGCCTTCG CAGGAACTGC TGGAAACCGG CATCAAGGTG ATCGACCTGA 350
TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTCGG TGGCGCCGGT 400
30 GTGGGCAAGA CCGTGAACAT GATGGAATC ATCAACAACA TCGCCAAGGG 450
CCACGGTGGT CTGTGCGGTG TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
GCAATGACTT CTATCACGAA ATGTTCGGACG CCGGCGTGGT CAACCAGGAG 550
TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
CCCGGGCAAC CGTCTGCGCG TGGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
35 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCCTGC 800
AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

40

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
55 (B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

60 GCCGTACCAC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
TCTGGTGCTG GAAGTTCAGC AGCAGCTGGG CGGCGGTATC GTACGTACCA 100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCTGAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGCGGT	GCGGGTGTAG	400
	GTAAAACCTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Neisseria canis*

(B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCTG	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGCG	GATGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTGTATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
	TAACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCTGAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAGCCG TGCCATTAC CAACTGCTC CGAAATTCGA CGAGTTGTCT 300
 TCAGTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTTCG AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGACTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30 2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAAC TCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCCGGTG TGCAGGTGTG 400
 55 GGTAAAACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTTA TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTGAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTTG CATTGACAGG CTTGACGATG GCAGAATATT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGTÇAGC	750'
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTTCG	850
ATCACTTCGG	GG				862

5

2) INFORMATION FOR SEQ ID NO: 749

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

	GGA	ACT	CCCCA	CGT	GAC	GCTA	TCCC	GCA	TGT	TTTT	GAT	GCA	TTAA	AATT	AG	50
25	TTG	AAA	ATGA	CCT	AAC	CTTA	GAAG	TTCA	AC	AACT	TTT	TGGG	GGAT	TGG	TGTA	100
	GTG	CGT	ACCA	TTG	CGA	TGGG	TAGT	TCAG	AT	GGAT	TAA	AAGC	GTGG	TAT	TGGC	150
	TGT	GA	ATAAT	ACCG	GAG	CTC	CGAT	TACT	TGT	TCCT	GTT	TGGC	CGTG	AACT	TT	200
	TGG	GTC	GTAT	CAT	GGA	TGTA	TTGG	GTA	ATC	CGGT	TGA	TGA	GGC	AGG	TCCG	250
	GTAA	ATGC	AT	CCA	ATA	CACG	TGCG	ATCC	AT	CAAG	AGG	CTC	CTA	AGT	TTGA	300
30	TGAG	CTTT	TCT	TCA	ACA	ACGG	AATT	ATTAG	A	AACT	TGG	CATT	AAG	GTT	TATCG	350
	ACT	TGTT	ATG	TCC	GTTT	TGCC	AAAG	GTGG	TGA	AAG	TAG	GTCT	GTTT	TGG	TGGT	400
	GCG	GGT	GTAG	GTAA	AAC	CGT	AAAT	ATG	ATG	GAG	TAA	TTA	ACA	ACAT	TGC	450
	CAAG	GCAC	AT	AGCG	GTTT	TGT	CTGT	GTTT	TGC	AGG	CGT	TGGG	GAAC	GTACT	CTC	500
	GTGA	AGGT	A	TGAC	TTCT	AT	CACG	AGAT	GTA	AAG	ATT	TCAA	CGT	ATT	TGGAC	550
35	AAAG	TGG	CAA	TGGT	TTAC	G	TCAG	ATGA	AC	GAAC	CTCC	AG	GCA	ACCG	TCT	600
	GCG	CGT	TGCT	TTG	ACCG	GTT	TGAC	TATG	GC	CGA	ATA	CTTC	CGT	GAC	GAAA	650
	AAG	ACG	AAAA	CGGT	AAAG	GT	CGCG	ACGT	AT	TGTT	CTTC	GT	GGAC	AAC	ATT	700
	TAC	CGT	TACA	CTTT	TGG	CCGG	TACG	GAAG	T	TCCG	CATT	TGC	TGGG	TCG	TAT	750
	GCCT	TCA	GCA	GTA	GGT	TACC	AACC	GAC	ATT	GGCT	GAA	GAA	ATGG	GTC	GTT	800
40	TGCA	AGAG	C	TATT	ACCT	CT	ACCC	GAC	AG	GCT	CTAT	TAC	TTCC			844

2) INFORMATION FOR SEQ ID NO: 750

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CGCG	ACG	GCTA	TTCC	GCA	TGT	TTAC	GAT	GCC	CTGA	AATT	TGG	ACG	AGA	AAC	G	50
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	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 31426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

35	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTCGC	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAACTC	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCGGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCAAACCG	GTTCCATTAC	TTCC		834

55 2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
15	GTTCGCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTC	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGTTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTTC	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCTGGAA	GTCCAACAGC	TTTTGGGTGA	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTAG	TTCAGACGGC	CTGAAACGCG	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTCGACGA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GGCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGAGG	CGTGGGCGAG	CGTACCCGCG	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

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2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GACTGTGAGC	150
AATACCGGTG	CGCCCATTAC	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
CATTGTGCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
30 TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGC	GGTGCCCGTG	400
TGGGTAAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCC CGGAAGG	500
TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GATAAAGTGG	550
35 CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
GCAATGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	ATCTACCGTT	700
ACACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
GCAGTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
40 GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

2) INFORMATION FOR SEQ ID NO: 755

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

60 CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
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430

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTAGTTCGTA	200
	CTATTGCAAT	GGGTAGTTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTTCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	CGGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGC GC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTTCGT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

CCCGTGATGC	TATTCCCATG	TATACGATGC	CCTGAAATTG	GTAGATAACG	50
ATCTGACCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15 TACCGGCGCT	CCGATTACTG	TTCCGGTGGG	GAAAGCCACC	TTGGGACGTA	200
TTATGGATGT	GTTGGGTAAT	CCGGTTGATG	AAGCAGGTCC	TGTTGTATCA	250
GAAGAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20 GGTAACACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
TAGTGGTTTG	TCTGTATTCT	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
ATGTTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25 ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
ACTCTGGCCG	GTAAGTGAAGT	GTCTGCACTG	TTAGGTCGTA	TGCCGTCTGC	750
AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50 TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55 TCCGTTTGCA	AAAGGCGGTA	AAGTAGGTCT	GTTCGGCGGT	GCCGGTGTGG	400
GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
TGGTGTACGG	TCAGATGAAT	GAGCCGCCGG	GCAACCGCTT	GCGCGTGGCT	600
60 TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAC	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

5

2) INFORMATION FOR SEQ ID NO: 759

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGGT	AAAGGTGGTA	AAGTAGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
GTAAAACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCTTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAAC	800
40 AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CAGCGAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTAATC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

20

2) INFORMATION FOR SEQ ID NO: 761

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Yersinia pestis*
- (B) STRAIN: KIM D27

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCAATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTCGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCTTC	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCCG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTTC	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCCCGCGA	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium sordellii*
- (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40	GAAGTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTCGC	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTCGG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 405 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
 (B) STRAIN: ATCC 19402

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTG	ACTCAAGCAG	GTTCAGAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATT	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

45

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium histolyticum*
 60 (B) STRAIN: ATCC 19401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
5	GAAAGATTCT	GGGGTTATAG	AGAAAACCTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTCTGC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCCTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCG	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTCG	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTCGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTCGTA	TCATGAACGT	CACCTGGTAC	CCCATGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTACG	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CTCCTTACGC	TCGTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTC	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCAC	GGTGGTTTCT	CTGTCTTCAC	TGGTGTCCGT	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCACTGTGT	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGATC	GAAGTGCTTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTTCG	ATCCCTCTG	CCGTCGGTTA	CCAGCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTGA	CTGACCCCTGC	900
	CCCCGCCACC	ACCTTCGCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCCG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTCGC	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT	CAAGGCTATC	TTGACTGGTG	AGGGTGACGA	CCTTCCCGAG	1300
GGTGAGTCTC	GACTATCTCC	GCATTCATAG	CGTATAACTG	ACA	1343

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2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT	GATTGTATGT	TCACCTGCAA	CATAAGACTT	CCCATTCTCC	50
ACTCTTTTCT	AACTCTTCAC	AGAACAACAT	TGCCAAGGCT	CACGGTGGTT	100
ACTCTGTCTT	CACTGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGATCTG	150
25 TACCACGAAA	TGCAGGAGAC	TGGTGTCAAT	CAGCTCGAGG	GTGAATCTAA	200
GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCAGGT	GCCCGTGCCC	250
GTGTCGCCCT	TACCGGTCTG	ACCATCGCCG	AGTACTTCCG	TGACGAGGAA	300
GGTCAGGATG	TGCTGCTCTT	CATTGACAAC	ATTTTCCGTT	TCACCCAGGC	350
CGGTTCTGAG	GTGTCTGCCC	TTCTTGGTCTG	TATCCCCTCC	GCTGTCTGGT	400
30 ACCAGCCAC	TCTGGCCGTC	GACATGGGTG	GTATGCAGGA	GCGTATTACC	450
ACCACCACCA	AGGGTTCCAT	TACCTCCGTC			480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

50 CTCGAACAAG	AYAACTTGCC	YGCCATTTTG	AACGCCCTTG	AAGTCAAGGA	50
YCACTCTGGT	GGACGTCTCG	TYCTCGAAGT	CTCTCAACAT	TTGGGTGAGA	100
ACACTGTCCG	TACTATTGCT	ATGGATGGTA	CTGAAGGTAA	GTTATGTYCA	150
TCCCANNGGA	TACAGTCARA	CAGMAATGTC	TAGTGGTTAT	AGCAGYAGCA	200
55 GATGATTGAC	CAATATGTTA	GGTCTTGTC	GGTGGTCAAA	AGGTTGTTGA	250
CACTGGTGCT	CCCATTACCA	TCCCCGTTGG	TAAGGAAGTC	CTTGGTCGTA	300
TCATCAACGT	TATTGGTGAA	CCCATTGATG	AACGTGGTCC	CATTGACGCC	350
AAGACTCACC	GTCCTATTCA	CGCTGAAGCT	CCCGAATTCG	TTGATCAATC	400
CCCCACTCCC	GAAATCCTCG	AGACTGGTAT	CAAGGTYGTC	GATTTGTTGG	450
60 CTCCTTATGC	TCGTGGTGGT	AAGATTGGTC	TCTTCGGTGG	TGCTGGTGTC	500

	GGTAAGACTG	TCTTGATTCA	AGAATTGATT	AACAACATYG	CCAAGGCTCA	550
	CGGTGGTTAC	TCTATCTTCT	GTGGTGTCTCGG	TGAACGTACT	CGTGAGGGTA	600
	ACGATTTGTA	CCATGAAATG	ATTGAAACCG	GTGTCATTCA	ATTGGAAGGC	650
	GAGTCCAAGT	GTGCTCTCGT	CTTTGGTCAA	ATGAACGAAC	CCCCAGGTGC	700
5	TCGTGCCCCG	GTCGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCCGTG	750
	ATGATGAGGG	TCAAGATGTC	TTGCTTTTCA	TTGATAACAT	TTTCAGATTG	800
	ACTCAAGCTG	GTTCTGAGGT	ATCTGCCCTT	TTGGGTGCGT	TTTCTTCCGC	850
	TGTCGGTTAC	CAACCCACTC	TTTCCACYGA	TATGGGTGGT	ATGCAAGAGC	900
	GTATTACTAC	CACCAAGAAC	GGTTCCATTA	CCTCCGTCCA	AGCTGTCTAC	950
10	GTCCCTGCTG	ATGATTTGAC	CGATCCTGCT	CCTGCCACCA	CTTTTGCTCA	1000
	CTTGGAATGCC	ACCACTGTCT	TGTCTCGTTC	CATCGCTGAA	TTGGGTATCT	1050
	AYCCCGCTGT	CGATCCTCTT	GATTCCAAGT	CTCGTATCCT	CGATCCCCGT	1100
	ATTGTCGGTG	ATGAGCACTA	CAAGGTTGCC	ACTGAAGTTC	AACAAATCCT	1150
	CCAAAACACTAC	AAGTCTCTCC	AAGA			1174

2) INFORMATION FOR SEQ ID NO: 772

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

	AGGAGCTTAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
35	ACTGGTGTCTG	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	100
	GCAAGAGACT	TCCGTCATTG	AGCTTGACSG	CGAGTCCAAG	GTCGCTCTCG	150
	TGTTCCGGTCA	GATGAACGAG	CCCCCGGGTG	CCCGTGCCCCG	TGTTGCCCTG	200
	ACTGGTCTTA	CCATCGCTGA	GTAATTCCGT	GATGCCGAGG	GTCAGGATGG	250
	TAAGTTCTAT	AACCTTTGTC	GCAAAGGTTT	CATTCTGGTC	GCTAACTTGC	300
40	TCAGTGCTCC	TGTTTCATCGA	CAACATTTTC	CGTTTCACCC	AGGCTGGTAT	350
	GGAGGTGTCT	GCCCTCCTCG	GTCGTATTCC	TTCTGCCGTC	GGTTACCAAC	400
	CTACTCTCGC	CGTCGACATG	GGTGGTATGC	AAGAGCGTAT	TACCACTACC	450
	AAGAAGGGAT	CCATTAC				467

2) INFORMATION FOR SEQ ID NO: 773

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

	TTGCCAAGGC	CCACGGTGGT	TACTCTGTCT	TCACTGGTGT	CGGTGAGCGT	50
	ACCCGTGAGG	GTAACGATCT	GTACCACGAA	ATGCAGGAAA	CCTCCGTCAT	100
5	TCAGCTTGAT	GGCGAGTCCA	AGGTCGCGCT	TGTCTTCGGT	CAGATGAACG	150
	AGCCCCCTGG	TGCCCCGTGCT	CGTGTCGCTC	TTACTGGTCT	TACCGTTGCC	200
	GAGTACTTCC	GTGATGAGGA	GGGTCAGGAT	GGTAAGTTAT	ATCGTTTTTA	250
	TTATCTTCTT	TGCCACCACC	CCTCTACGAA	TCCATGCCTC	CGTTGGTGAA	300
	GGCATCGTTT	GTAGGGCGGG	TCGGAGTTTG	CGGCAATTTC	TGCCGTCGGC	350
10	TTGAAGCCGC	GGATGCCCCG	TGTTTGACGC	GTATCGATGC	TAACAACAAT	400
	GACAACAGTG	CTTCTCTTCA	TTGACAACAT	TTTCCGATTC	ACCCAGGCCG	450
	GTTCCGAGGT	GTCTGCCCTT	CTCGGTCGTA	TTCCCTCTGC	CGTCGGTTAC	500
	CAGCCCCTC	TTGCCGTAGA	CATGGGTGCC	ATGCAGGAAC	GTATTACCAC	550
15	CACCAAGAAG	GGTTCGATTA	CCTCCGTC			578

2) INFORMATION FOR SEQ ID NO: 774

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1123 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Rhizopus oryzae*
 - (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

	AACTTACCYG	CTATCTTGAA	CGCTCTCGAA	GTCCAAGATC	ACTCTGGTGG	50
35	ACGTCTTGTC	CTTGAAGTTC	GCTCAACACT	TGGGTGAAAA	TACTGTCCGT	100
	ACTATTGCTA	TGGATGGTAC	TGAAGGTAAG	CTATACTATA	ACCGTKTTAT	150
	CCGAGTATGA	TATTAACCTG	AAAAAAGGTC	TCGTTCGTGG	TCAAAAGGTT	200
	ATTGACACTG	GTGCTCCCAT	TACCATTCCT	GYTGGTAAGG	AAGTTCTCGG	250
	TCGTATCATT	AACGTCATTG	GTGAACCCAT	CGATGAACGT	GGTCCTATCA	300
40	ACGCCAAGAG	CCAACGTCCC	ATTCACGCCG	AAGCTCCCGA	ATTCGTTGAC	350
	CAATCTCCTA	CTCCCGAAAT	TCTTGAAACT	GGTATCAAGG	TTGTCGACTT	400
	GTTGGCTCCT	TATGCTCGTG	GTGGTAAGAT	TGGTCTTTTC	GGTGGTGCTG	450
	GTGTCGGTAA	GACTGTGTTG	ATTCAAGAAT	TGATTAACAA	CATCGCCAAG	500
	GCTCACGGTG	GTTACTCTAT	TTTCTGTGGT	GTCGGTGAAC	GTACTCGTGA	550
45	AGGTAACGAT	CTTTACCACG	AAATGATTGA	AACTGGTGTC	ATCAAGCTCG	600
	ATGGTGACTC	CAAGTGTGCT	CTTGTCTTTG	GTCAAATGAA	CGAACCCCCA	650
	GGAGCTCGTG	CCCGTGTTGC	CTTGACTGGT	TTGACCATTG	CTGAATACTT	700
	CCGTGATGAT	GAAGGTCAAG	ATGTGTTGCT	TTTCATTGAT	AACATTTTCC	750
	GTTTCACCCA	AGCTGGTTCW	GAAGTATCTG	CCCTTTTGGG	TCGTATTCCC	800
50	TCCGCTGTCTG	GTTACCAACC	CACCTCTTCT	ACTGATATGG	GTGGTATGCA	850
	AGAACGTATT	ACAACCACCA	AGAACGGTTC	CATTACATCC	GTCCAAGCTG	900
	TCTACGTCCC	TGCTGATGAT	TTGACCGATC	CTGCTCCCGC	CACCACTTTT	950
	GCTCACTTGG	ATGCCACCAC	TGTCTTGTCT	CGTTCCATTG	CCGAATTGGG	1000
	TATTTACCCT	GCCGTCGATC	CTCTTGAYTC	CAAGTCTCGT	ATCTTGATC	1050
55	CTCGTATCGT	TGGTGACGAA	CACTACAAGG	TCGCTACCGA	AGTTCAACAA	1100
	ATCCTTCAAA	ACTACAAGTC	TCT			1123

60 2) INFORMATION FOR SEQ ID NO: 775

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

```

15  ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT      50
    GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG      100
    AAATGCAGGA GACTTCGGTC ATTCAAGCTCG AGGGCGAGTC CAAGGTCGCG      150
    CTTGTGTTTC GTCAGATGAA CGAGCCCCC GGTGCCCGTG CCCGTGTCGC      200
20  CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG      250
    ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG      300
    ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG      350
    GTTCCGAGGT TTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC      400
    CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC      450
25  GACTCAGAAG GGCTCGATTA CCTCGGT      477
  
```

2) INFORMATION FOR SEQ ID NO: 776

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

```

45  TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC      50
    TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT      100
    TCGAGTATTA ATTGTTTTTA TAGAACAACA TTGCCAAGGC TCACGGTGGT      150
    TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT      200
    CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GGCGAGTCCA      250
50  AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC      300
    CGTGTTGCTC TTA CTGTTT GACCATTTGCT GAGTACTTCC GTGATGAGGA      350
    AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT      400
    TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT      450
    CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCC      500
55  TGCTTGGTTCG TATCCCATCT GCCGTCGGTT ACCAACCCAC TCTTGCCGTC      550
    GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT      600
    TACCTCCGTC      610
  
```

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

```

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCAAGAAA CAGAAGCTAG      50
GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTTCG      100
AGTATTAATT ATTTTATAG AACAACATTG CCAAGGCTCA CGGTGGTTAC      150
TCTGTCTTCA CTGGTGTCCG AGAGCGTACC CGTGAAGGAA ACGATCTCTA      200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG      250
TCGCCCTGGT CTTCCGCCAG ATGAACGAGC CCCAGGTGC CCGTGCCCGT      300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG      350
TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTT TTCAAGAAAT      400
TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT      450
TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC      500
CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT      550
GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC              593

```

2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

```

CCGTGGTCAA GAAGTTATTG ACACTGGTGC CCCAATTACC ATTCCTGTTG      50
GTCGTGGTAC TCTTGGTAGA ATTATCAACG TCATTGGTGA ACCAATTGAC      100
GAACGTGGCC CTATCAAGGC TTCTAAGTAT GCTCCTATCC ATACTGAACC      150
ACCAACCTTT GCTGAACAAT CTACTTCTGC TGAAGTTCTT GAAACCGGTA      200
TCAAGGTTGT CGATCTTCTT GCTCCTTACG CCCGTGGTGG TAAGATTGGT      250
CTTTTCGGTG GTGCTGGTGT CGGTAAGACT GTCTTCATTC AAGAACTTAT      300
TAACAACATT GCCAAGGCTC ACGGTGGTTT CTCTGTCTTC ACTGGTGTCG      350
GTGAAAGAAC CCGTGAAGGT AACGATCTTT ACCGTGAAAT GAAGGAAACT      400
GGTGTCAATCA ACCTCGAAGG TGACTCCAAG GTCGCTCTCG TTTTCGGTCA      450
AATGAACGAA CCTCCAGGTG CCCGTGCCCC TGTCGCTTTG ACTGGTCTTA      500
CCATTGCCGA ATACTTCCGT GATGAAGAAG GACAAGATGT CTTGCTTTTC      550
GTTGACAACA TTTTCAGATT CACCAAGCC GGTTCGAAG TCTCTGCTCT      600
TTTGGGTCGT ATTCCATCTG CCGTCCGTTA CCAACCTACC CTTGCTACCG      650

```

	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700
	ACATCTGTCC	AAGCCGTCTA	TGTCCTCAGCA	GACGATTGTA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTT	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Cladophialophora carrionii*
- (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	TCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCCG	600
	CGGTCGTGTT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTT	GTCGTGGAAA	CGTTGCTGGT	GACTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCAGGT	CATCGTCCTC	850
	AACCACCCTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTACCGGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

```

10 TACTTGTAAG TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT      50
   CTTCTTTCAT CAAGAAGATT GGTTACAATC CTAAATCCGT TCCTTTCGTY      100
   CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT      150
   GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG      200
15 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT      250
   TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG      300
   TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG      350
   GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC      400
   GTTGAAATGC ATCACGAACA ATTAGAACAA GGTGTTCTCT GTGACAACGT      450
20 TGGTTTCAAC GTCAAGAACG TTTCCGTTAA GGATATCCGT CGTGGTAACG      500
   TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC      550
   GCTCAAGTTA TCGTCTTGAA CCACCCTGGT CAAATTGGTG CTGGTTATGC      600
   CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT      650
   TATTAGAAAG GATCGATCGT CGTTCCGTA AGAAACTCGA AGATGCTCCT      700
25 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA      750
   GC

```

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

```

45 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC      50
   TCATCAAGAA GGTCGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC      100
   TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCTTG      150
   GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC      200
50 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG      250
   CCCCTCCGCC TTCCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC      300
   GGTCCTCGTC GGTCTGTGTC AGACCGGTAT CATCAAGCCC GGTATGGTCG      350
   TCACCTTCGC CCCCGCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG      400
   CACCACGAGC AGCTTACTGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA      450
55 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGATAAC GTTGCCGGTG      500
   ACTCCAAGAA CGACCCCCCC AAGGGTTGCG AGTCCTTCAA CGCCCAGGTC      550
   ATCGTCCTCA ACCACCCTGG TCAGGTCGGT GCCGGTTACG CCCCAGTCCT      600
   TGACTGCCAC ACTGCCACA TTGCCTGCAA GTTCTCCGAG CTCCTCGAGA      650
   AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC      700
60 AAGTCCGGTG ACGCCGCCAT CGTCAAGA

```

2) INFORMATION FOR SEQ ID NO: 782

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

20	TGAAGTCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
	CGCTAACCTA	TTCAACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAATCATG	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
25	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
30	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
35	ACGAGCAGCT	TCCCGAGGGT	CTCCCCGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGCAACGTCG	CCGGTGACTC	850
	CAAGAACGAC	CCCCCAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
40	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
	GAGGCCTTCA	CCGACTACCC	CCCTCTTGGA	CGTTTCGCCG	TCCGT	1145

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTTCGAGAC	CCCCAAGTAC	ATGGTCACCG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATT	ATAGTTGCGA	CAAGTAACTA	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATT	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTCTGTCCT	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAAGTGGCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTCAG	GGTGTTCCCG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
20	TCGTCCTCAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Mucor circinelloides*
- (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTTCG	GTTGAACTG	GTACTATCAA	GGCTGGTATG	350
	TTTGTCACCT	TGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTGTA	400
	AATGCATCAC	GAAACCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAACTCATT	650
	GAGAAGATTG	ATCGTCGTTT	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTTT	ACATAATTTG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTA G GT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

5

2) INFORMATION FOR SEQ ID NO: 785

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
- (B) STRAIN: ATCC 38561

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

25	GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
	TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCCT	100
	GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
	TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
	GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30	GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
	AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
	TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
	TCGAGGCCAT	CGACGCGATT	GACCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35	CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
	GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
	CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
	CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCG	GCTTCAACGT	750
	CAAGAACGTC	TCCGTCAAGG	AGGTTCTGTCG	TGGAAACGTT	GCCGGTGACT	800
40	CCAAGAATGA	CCCCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
	GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
	TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
	TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
	TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45	TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*

60

448

(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

5	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCYAGY	CGTCCCACCG	250
10	ACAAGCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300
	GGCACGGTTC	CCGTCGGTCG	TGTYGAGACC	GGTRCCATCA	AGGGTGGCAT	350
	GGTCGTCACC	TTCCCCCCCCG	CTGGTGTCAC	CACTGAGGTC	AAGTCCGTCG	400
	AGATGCACCA	CGAGCAGCTC	GCCGAGGGTS	TCCCCGGTGA	CAACGTCGGC	450
	TTCAACGTCA	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GCAACGTTGC	500
15	CGGTGACTCC	AAGAACGACC	CCCCCAAGGG	CTGCGACAGC	TTCAACGCCC	550
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGCGCCGG	CTACGCGCCS	600
	GTCCTSGACT	GCCACACTGC	TCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	650
	CGAGAAGATC	GACCGCCGTT	CCGGCAAGTC	CATCGAGTCC	GGCCCCAAGT	700
	TCATCAAGTC	TGGTGACGCC	GCCATCGTCA	AGATGGTTCC	CTCCAAGCCC	750
20						

2) INFORMATION FOR SEQ ID NO: 787

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
- (B) STRAIN: ATCC 32330

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	50
40	AGTTCGAGAC	CCCCAAGTAC	CACGTCAACG	TCATTGATGC	CCCCGGCCAT	100
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CTGACTGCGG	150
	TATCCTCATC	ATTGCCGCCG	GTACTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TTGCCTTCAC	CCTCGGTGTC	250
	CGTCAGCTGA	TCGTGCGCCAT	CAACAAGATG	GACTCGACCA	AGTACTCTGA	300
45	GGCCCCGTTAC	AACGAAATCG	TCAAGGAGGT	CTCCACCTTC	ATCAAGAAGA	350
	TCGGTTTCAA	CCCCAAGTCC	GTTCCCTTCG	TCCCCATCTC	TGGCTGGAAC	400
	GGTGACAACA	TGTTGGAGGA	GTCCTCCAAC	ATGCCCTGGT	TCAAGGGCTG	450
	GAAGAAGGAG	ACCAAGGCTG	GCGAGAAGTC	CGGCAAGACC	CTCCTTGAGG	500
	CCATTGACAA	CATTGACCCC	CCGGTCCGTC	CCTCGGACAA	GCCCCTCCGT	550
50	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATCGGCA	CAGTCCCCGT	600
	CGGTCGTGTC	GAGATGTTG	TCATCAAGGC	TGGTATGGTC	GTGACCTTCG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
	CAGCTCGTCG	AGGGTGTTCC	CGGTGACAAC	GTCGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTC	AAGGATATCC	GCCGTGGTAA	CGTCTGCTCT	GACTCCAAGA	800
55	ACGACCCCGC	CAAGGAGTCT	GCCTCGTTCA	CCGCCAGGT	CATCGTCCTG	850
	AACCACCCCG	GTCAGATCGG	TGCCGGTTAC	GCCCCGGTTC	TTGACTGCCA	900
	CACCGCTCAC	ATTGCCTGCA	AGTTCGCTGA	GCTCCTCGAG	AAGATCGACC	950
	GTCGTTCCGG	YAAGAAGCTC	GAAGAGTCCC	CCAAGTTCGT	CAAGTCGGGT	1000
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1050
60	CTACACTGAG	TACCCCCCTC	TTGGCCGTTT	CGCC		1084

2) INFORMATION FOR SEQ ID NO: 788

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCTTT	100
	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAAC TAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTCGAGGCT	250
25	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCT	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCATGGT	500
30	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACCC	GTCCTACCGA	600
	CAAGCCCCTY	CGTCTCCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAAGTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTCACCT	TCGCCCTGCG	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
35	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CACATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
40	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTCGAAGCCA	ACCCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
	TGTGCGTTGA	GGCTTTCACT	GACTACCCCC	CACTTGGTCG	TTTCGCCGTC	1150
	CGTGA					1155

2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCCTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAACTTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTTCGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCTCCG	TCTCCCACTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCACCTGA	CTACCCCCCA	CTTGGTTCG		1138

2) INFORMATION FOR SEQ ID NO: 790

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACCTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCTTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCAGTA	350
	TGGTTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

60

2) INFORMATION FOR SEQ ID NO: 791

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Aspergillus fumigatus*
 15 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
20	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTTCGC	GAATAGGCCC	100
	CAGACTCGTG	AGCATTTGCT	GCTCGCCCGC	CAGGTTGGTG	TCCAGAAGAT	150
	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACTGGTCTGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
25	ACGCCGTGAC	GACATCGGTA	AAGACAGAAT	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTTCTTG	400
	ATGTCTGTCTG	AGGAAGTGTT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCGAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
30	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAACT	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCGTGGTATG	GTCATTGCTG	650
	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCGTA	GGCTTCGGTG	CCAACTACCG	750
	TCCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTC	800
35	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

2) INFORMATION FOR SEQ ID NO: 792

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

	CGTTGTGCA	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACG	50
	GATGAAAGGA	TTTGACGTTT	CTAACATCAT	TCTAGGCCTC	AGACCAGAGA	100
60	ACATTTGCTC	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	150

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	400
	GGAAGTGTTT	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGGTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAACCTC	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTCG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35 2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50 GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGCACGC GATGTGGCAG

20

2) INFORMATION FOR SEQ ID NO: 796

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25

GGTCCAATGC CWCAAACWAG A

21

2) INFORMATION FOR SEQ ID NO: 797

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

40

CATTAAGAAT GGYTTATCTG TSKCTCT

27

2) INFORMATION FOR SEQ ID NO: 798

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

50

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

TGGTTGTCCC AGCCGATCGT TT

22

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T

21

25 2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

40 GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

60 ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

TTGCCATTTC TGGTTTCGTT

20

2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

ACTTCAGTGG TAACACCAGC

20

2) INFORMATION FOR SEQ ID NO: 804

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

CCTGGGACGG CCTCTGGCAT

20

2) INFORMATION FOR SEQ ID NO: 805

(i) SEQUENCE CHARACTERISTICS:

456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTCCTA TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

50

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTTGC

20

55

2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

458

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

10 GTIACIGGIT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA

22

2) INFORMATION FOR SEQ ID NO: 814

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

40

GCIGGCACGT ACACIGCCTG

20

45 2) INFORMATION FOR SEQ ID NO: 815

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

55

TGGTGATYT CKACRGACTT

20

60

2) INFORMATION FOR SEQ ID NO: 816

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

AGCCGGGCTG GATCTTCTTC

20

2) INFORMATION FOR SEQ ID NO: 819

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

TCGAGCTTCT GGAGGAAGAG

20

5 2) INFORMATION FOR SEQ ID NO: 820

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C

21

25 2) INFORMATION FOR SEQ ID NO: 821

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A

21

2) INFORMATION FOR SEQ ID NO: 822

45 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

GAGCGGTATG AYGAGATTGT

20

2) INFORMATION FOR SEQ ID NO: 824

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

GGCTTCTGCG GCACCATGCG

20

2) INFORMATION FOR SEQ ID NO: 825

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

ATGAGCARCG SAACCATCGT TCAGTG

26

2) INFORMATION FOR SEQ ID NO: 826

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

462

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 446 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

35 2) INFORMATION FOR SEQ ID NO: 828

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 445 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCTTG	100
	AATTAAAAGA	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
20 TATTGACCCA	AAAAGTGGGG	AAAGTTTAAT	GAAGAGAACA	GTAATTATAG	150
CTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAAG	GAAATGTCAG	300
GTAAGCTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTACTTAGGA	350
25 TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

2) INFORMATION FOR SEQ ID NO: 830

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
50 GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTC	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40

	CCAACTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
50	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

50

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

```

10  TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT 50
    GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG 100
    CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTCAGG 150
    TTTATGAGGA AACATCAGGG ATCGGTCCAG GAGAACCAGT AGTGACTACT 200
    GGTGTGCTTT TGTCGGTTCG GTTAGGCCCG GGCCTGATTT CAGAAATGTT 250
    TGACGGTATT CAGCGACCGC TTGATCGTTT TCAAAAAGCA ACGGACAGCG 300
15  ACTTTTTTAAT CCGTGGTGTG GCTATCCCAA GTCTTGATCG AAAGGCTAAG 350
    TGGGCATTTA TTCCCAAGCT AAGTGTTGGT CAAGAAGTAG TTGCAGGTGA 400
    TATTTTAGGA ACTGTGCAAG AAACAGCTGT CATTGAGCAC CGTATCATGG 450
    TTCCTTATAA AGTTTCAGGG ACCTTGGTGG CTATTCATGC AGGGGACTTC 500
    ACAGTAACAG ATACAGTTTA TGAAATTAAG CAGGAAGACG GTTCCATTTA 550
20  CCAAGGTAGC CTCATGCAGA CTTGGCCAGT TCGTCAAAGT CGCCCTGTTG 600
    CTCAAAAGCT TATCCCAGTC GAACCTTTGG TTACAGGTCA ACGGGTTATT 650
    GACACCTTTT TCCCTGTTAC AAAAGGTGGT GCCGCTGCCG TTCCTGGACC 700
    ATTTGGGGCA GGAAAAACAG TTGTGCAGCA TCAAATAGCT AAATTTGCCA 750
    ACGTTGATAT TGTTATTTAT GTCGGTTGTG GGAACGCGG CAACGAGATG 800
25  ACCGACGTTT TGAATGAGTT TCCAGAGTTA ATTGACCCAA ATACAGGCCA 850
    GTCCATTATG GAGCGCACGG TGTTAATTGC AAACACCTCT AATATGCCAG 900
    TAGCAGCGCG TGAAGCGTCG ATTTACACAG GTATTACCAT TGCCGAATAT 950
    TTCCGTGATA TGGGCTATTC TGTGGCTATC ATGGCAGACT CGACATCACG 1000
    TTGGGCAGAA GCTCTGCGCG AGATGTCAGG ACGCCTACAA GAAATGCCTG 1050
30  GTGATGAAGG CTACCCGGCT TACTTAGGGA GTCGTATTGC CGAATATTAT 1100
    GAACGGGCTG GTCGTGTTCC GACCTTGGGA AGTCAAGAAC GTGAGGGAAC 1150
    CATTACAGCC ATCGGCGCGG TTTCTCCTCC TGGAGGGGAT ATTTACAGAGC 1200
    CTGTCACTCA AAACACCCTT CGGATTGTCA AAGTTTTCTG GGGGCTCGAC 1250
    GCGCCTCTTG CGCAACGGCG TCACTTCCCA GCGATTAAC TGGCTGACGTC 1300
35  TTATTCATTG TATCAAGATG ATGTAGGAAG CTATATTGAC CGTAAACAGC 1350
    AATCTAATTG GTCCAACAAG GTAACTCGTG CCATGGCTAT TTTGCAGCGT 1400
    GAAGCCAGTC TAGAAGAAAT TGTACGCTTG GTGGGGCTTG ATTTACTGTC 1450
    TGAACAAGAT CGTTTGACCA TGGCTGTTGC CCGGCAAATT CGGGAGGATT 1500
    ATCTCCAGCA AAATGCCTTT GATTGCGTGG ATACCTTTAC TTCCTTTCCG 1550
40  AAACAAGAGG CCATGCTAAC CAATATTTTG ACCTTTAATG AGGAAGCCAG 1600
    CAAAGCCCTT TCTTTGGGAG CTTATTTTAA TGAGATTATG GAAGGCACTG 1650
    CTCAGGTACG CGATCGCATC GCACGCAGCA AATTTATCCC AGAAGAAAAC 1700
    TTAGAGCAGA TTAAAGGGCT TACTCAGAAG GTTACCAAAG AGATTACCA 1750
    CGTTTTAGCA AAGGGAGGAA TTTAGATGAG CGTTCT 1786
45

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2) INFORMATION FOR SEQ ID NO: 834

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bovis*

(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

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5  TATCTCACGT AAGTTTTTGC GCGGCGGTTA TATATCACTC CAGGCCCTGG 50
   CTAAGTACGC TAATACTGAC GTTACTGTCT ATGTGGGATG TGGAGAGCGT 100
   GGAAACGAGA TTGCGGAGGT GCTTAAGGAG TTCCCTGAGC TGAAGACCAA 150
   GGTTGATGGC AAGGAAGTGA GCATTATGAA ACGCACTTGC TTGGTGGCCA 200
   ATACTTCAAA CATGCCAGTG GCCGCCAGGG AGGCTAGTAT CTACACTGGC 250
   ATTACCCTAT GTGAATACTT CAGGGATATG GGATACAACG CCTGTGTGAT 300
10 GGCGGATTCC ACCAGTCGTT GGGCTGAGGC TTTGCGTGAG ATATCAGGTC 350
   GTTTAGCTGA GATGCCTGCT GATTCAAGTT ATCCCGCCTA CCTTGCTTCT 400
   AGGCTTTCGG CGTTCTATGA GCGTGCTGGT ACAGCTGAGT GTATTGGAAC 450
   ACCACTTCGT GAAGGTTTCA TTACCATTGT TGGTGCTGTA TCTCCACCA 499

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15

2) INFORMATION FOR SEQ ID NO: 835

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20  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 464 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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25  (ii) MOLECULE TYPE: Genomic DNA

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     (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Cryptosporidium parvum

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

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   TTTCTCAAGC TTTGAGTAAA TATAGTAACT CTGATGTTAT TATTTACATT 50
   GGTGTGTGGAG AAAGAGGAAA TGAAATGGCA GAAGTTCTTA CAGAATTTCC 100
   TGAGCTTTAT ACTATGGTTG ATGGAAAGAA GGAGTCAATT ATGCAAAGAA 150
35  CTTGTTTAGT AGCTAATACA TCAAATATGC CTGTCGCTGC TAGAGAAGCT 200
   TCCATCTACA CTGGTATTAC ACTTTCTGAA TACTTTAGAG ATATGGGATG 250
   TAATGTTTCT ATGATGGCAG ATTCAACTTC TCGTTGGGCT GAAGCTCTTA 300
   GAGAAATTTC TGGTAGATTA GCTGAAATGC CTGCAGATTC GGGTTACCCA 350
   GCATATTTAG GCGCCAGACT TGCTTCATTC TATGAAAGAT CAGGAAGAGT 400
40  TAAATGTATG GTTTCCCCAG ATAGAGAAGG TACAGTAACA ATTGTTGGTG 450
   CAGTTTCTCC ACCT 464

```

45 2) INFORMATION FOR SEQ ID NO: 836

3)

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     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 446 bases
         (B) TYPE: Nucleic acid
50  (C) STRANDEDNESS: Double
         (D) TOPOLOGY: Linear

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     (ii) MOLECULE TYPE: Genomic DNA

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55  (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Leishmania infantum
         (B) STRAIN: MOU

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

60

	GCCCTCTCCA	AGTACTCCAA	CTCCGATTGC	GTCATCTATG	TCGGCTGCGG	50
	CGAGCGCGGT	AATGAGATGG	CCGAGGTGCT	CATGGAGTTC	CCGACCCTGA	100
	CGACCGTGAT	CGATGGCCGC	GAGGAGTCGA	TCATGAAGCG	CACCTGCCTC	150
	GTGGCGAACA	CCTCGAACAT	GCCAGTCGCA	GCCCGTGAGG	CCTCTATTTA	200
5	CACCGGCATC	ACCCTGGCCG	AGTACTACCG	TGATATGGGC	AAGCATATCG	250
	CCATGATGGC	TGACTCGACG	TCTCGCTGGG	CCGAGGCGCT	TCGTGAGATT	300
	TCGGGTCGTC	TGGCGGAGAT	GCCGGCGGAT	GGTGGCTACC	CCGCCTACCT	350
	CAGCGCTCGT	CTCGCCTCCT	TCTACGAGCG	CGCCGGCCTC	GTCACCTGCA	400
10	TCGGCGGGCC	GAAGCGCCAG	GGCTCCGTCA	CGATCGTCGG	TGCCGT	446

2) INFORMATION FOR SEQ ID NO: 837

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

	TTAGTCAGGC	CCTCTCCAAG	TACTCCAAC	CCGACTGCGT	CATCTATGTC	50
30	GGCTGCGGCG	AGCGCGGTAA	TGAGATGGCT	GAGGTGCTCA	TGGATTTCCC	100
	AACTCTGACG	ACCGTGATCG	ATGGTCGCGA	GGAGTCCATC	ATGAAGCGCA	150
	CCTGCCTCGT	GGCAAACACT	TCGAACATGC	CAGTCGCAGC	CCGCGAGGCC	200
	TCTATTTACA	CCGGCATCAC	CCTGGCCGAG	TACTACCGTG	ATATGGGCAA	250
	GCATATTGCC	ATGATGGCCG	ACTCGACATC	TCGCTGGGCC	GAGGCGCTTC	300
35	GTGAGATTTT	CGGTCGTCTG	GCGGAGATGC	CAGCCGATGG	TGGCTACCCT	350
	GCCTACCTCA	GCGCTCGTCT	CGCCTCCTTC	TACGAGCGCG	CCGGCCTCGT	400
	CACCTGCATC	GGCGGGCCGA	AGCGCCAGGG	CTCCGTCACG	ATCGTCGGTG	450
	CTGTGT					456

40

2) INFORMATION FOR SEQ ID NO: 838

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: MOU-2

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

	AGGCCCTCTC	CAAGTACTCC	AACTCCGACT	GCGTCATCTA	CGTCGGCTGC	50
	GGCGAGCGCG	GTAATGAGAT	GGCCGAGGTG	CTCATGGAGT	TCCCGACCCT	100
60	GACGACTGTG	ATTGATGGCC	GTGAGGAGTC	GATCATGAAG	CGGACCTGCC	150

TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5 CTTAGTGCTC	GTCTTGCCCTC	CTTCTACGAG	CGTGCCGGCC	TCGTCACCTG	400
CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 437 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
(B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

25	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCGCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
35	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

55	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTTCGAGTCG	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGCTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

60 2) INFORMATION FOR SEQ ID NO: 842

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

```

15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA      50
   AGTTCGAGTC GCCCAAGTCT GTGTTCACGA TCATCGACGC CCCCGGCCAC      100
   CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC      150
   CGTCCTTGTC ATTGCGTCAT CGCAGGGTGA GTTTGAGGCG GGCATCTCGA      200
20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG      250
   AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAACCT      300
   CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCG GCGTACCTGA      350
   AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC      400
   TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA      450
25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC      500
   CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC      550
   GGTATCGGCA CCGTGCCGGT CGGTGCGGTG GAGACGGGCA CGATGAAGCC      600
   CGGCGACGTG GTGACGTTTG CGCCCGCCAA CGTGACGACG GAGGTGAAGT      650
   CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC      700
30 GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG AAGGACATCC GCCGTGGCAA      750
   CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA      800
   CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT      850
   GCGCCGGTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA      900
   GATCGAGTCC AAGATCGACC GCCGCTCCGG CAAGGAGCTT GAGAAGAACC      950
35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG     1000
   AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT     1050
   TGCCGTGCGT GA                                     1062

```

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

```

60 TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG      50
   AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
   GGTATTACTA TAAATTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
   TTACGGTCAC GTGGACTGTC CAGGTCACTC TGATTATGTG AAGAACATGA      200

```

	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTTCGTGA	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCGT	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGACG	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

20

2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 943 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCAGCG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTGCGC	550
	ACCGGCGACA	CAACCAAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGCAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGGGA	GGAGCTGAAC	AAGAAATTCTG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

472

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

```

15  CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
    GCGAGCATCT CTTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
    TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
    CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA      200
20  CGCCCATCGT GCGCGGCTCG GCCCTCAAAG CCGTCGAGGG CGACGCGAAG      250
    TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCACG AATGGATCCC      300
    CGACCCGCCG CGCAACACAG ACAAGCCTTT CTTATGGCC ATTGAGCACG      350
    TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
    GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG      450
25  CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA      500
    CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCTGGC      550
    ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT      600
    AATGGCGGCA ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650
    TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTCAGCCCC      700
30  CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT      750
    GAGCTTCCCG GAGGCGGAGA AGCACC GCGA GGAGCTCAAC AAGAAATTCG      800
    GCCGCGGCCG CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC      850
    GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACCGCGAGC TGATCCTGAC      900
    GCTGGCGTAC CCGATGCCCA TTGACAAGGG TCTGAAGTT      939
35

```

2) INFORMATION FOR SEQ ID NO: 846

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

```

55  CATTGTGGTG GCGGCCACCG ACGGCGTCAT GCCGCAGACA CGCGAGCACC      50
    TCCTGATCTG CTCGCAGATC GGGCTTCCGG CGCTCGTAGG GTTCATCAAC      100
    AAGGTGGACA TGACGGACGA GGACACGTGC GACCTGGTGG ACATGGAGCT      150
    GCGCGAGCAG CTGGAGAAAT ACAAGTTTCC GCGGAGGAG ACGCCAATCG      200
    TGC GCGGCTC AGCCCTCAA GCCGTCGAGG GCGATGCGAA GTACGAGGAG      250
    AACATTCTCG AACTGGTGCG GAAGTGTGAC GAGTGGATCC CTGACCCGCC      300
60  GCGCAACACA GACAAGCCTT TCCTTATGGC CATCGAGCAC GTTTACGAGA      350

```

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCGTGA	CCGGCCGCGT	CGATCAAGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCTG	GACCGGCGAC	550
5	ACGACCAGTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACC GCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCGATGCCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

15

2) INFORMATION FOR SEQ ID NO: 847

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGTGCAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCGCA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCGGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTGA	AAAGGGTCTG	AAGTTCACC		939

55

2) INFORMATION FOR SEQ ID NO: 848

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 933 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

```

10 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC      50
   AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG      100
   GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGCTGGA      150
   GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC      200
   TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG      250
15 GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA      300
   GCCTTTTCCTC ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA      350
   AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC      400
   ACAGACGCCG AGCTGGCCGG CTTCAGCGCC AAGAAGGCGA CAGTCAAAGT      450
   GACGGGCATC GAGATGTATC ACAAGACACT CAATGAGTGC ATGCCCGGCG      500
20 ACTCTGTCGG TGTCAGCATC GTCGGTACCG GTGACACGAC CAGCTTATCC      550
   AAGGATAATG TTGAGCGCGG TAGGTAATG GCGGCAACGG GTAGCACGAA      600
   CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG      650
   GTGGCCGCCA CACCGGGTTC AGCCCCACT ACCGCCGCA GCTCTTCTTC      700
   CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA      750
25 CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA      800
   AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTTG CTGCATGCCA      850
   GCGGATAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA      900
   CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CGG                      933

```

30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
45 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

```

CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
50 TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
   CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
   CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
   TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AGTGGATCCC      300
   CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATCGAGCACG      350
55 TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
   GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG      450
   CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA      500
   CGCTGAGCGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTGCGC      550
   ACCGGCGACA CGACCAGTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT      600
60 AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650

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	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCA S CCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
	CCGCGGGCCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCTCT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCGCA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
45	GCGTACCCGA	TGCCCAT				918

2) INFORMATION FOR SEQ ID NO: 851

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 60 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

5	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCATCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCAGAC	AATGGATCCC	300
10	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGTCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGG	550
15	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC CGCA	GGAGCTCAAC	AAGAAATTCG	800
20	GCCGCGGCCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAGAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 912 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: <i>Leishmania tarentolae</i>
(B) STRAIN: MOU-2

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

45	TCATTGTGGT	GGCCGCCACC	GACGGCGTCA	TGCCGCAAAC	ACGGGAGCAC	50
	CTTTTGATCT	GCTCGCAGAT	CGGGCTGCCG	GCGCTCGTAG	GGTTCATCAA	100
	CAAAGTGAGC	ATGACAGACG	AAGACACGTG	CGACCTGGTA	GACCTGGAGG	150
	TGCGTGAGCA	GCTGGAGAAG	TACAAGTTTC	CGGCAGAGGA	AACACCAATC	200
	GTGCGTGGCT	CGGCCCTCAA	GGCCGTTGAG	GGCGATGCAA	AGTACGAGGA	250
	GAACATCCTC	GAAGTGGTGC	GGAAGTGC GA	CGAGTGGATC	CCAGACCCGC	300
	CACGCAATAC	GGACAAGCCT	TTCCTTATGG	CCATTGAACA	CGTGTACGAG	350
	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
50	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GACACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATGTGGG	GCACTGGYGA	550
	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTACTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
55	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCACTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAACTCA	ATAAGAAATT	CGGCCGCGGC	800
	CCCGAGGAGG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
60	ACCCGATGCC	TA				912

2) INFORMATION FOR SEQ ID NO: 853

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

20	ATTCTTGTGG	TGGCAGCTAA	CGACGGATGC	ATGCCGCAGA	CGCGTGAGCA	50
	CCTGCTTATT	TGTTTCGAGA	TTGGCCTTCC	TGCTCTTGTA	TGCTTTATCA	100
	ATAAGTGTGA	CATGATGCAA	GGGCAGGAGG	AAATGATTGA	ACTTGTTGAA	150
	ATGGAGGTAC	GTGAACTTTT	GGAGAAAGTAC	AAGTTCCCTG	CGGAGGAGAC	200
	GCCATTTGTG	CGGGGGTCTG	CGGTGAAGGC	ATTGGAGGGT	GATGCTGAAA	250
25	ATGAAGGAAA	GATTTTGGAG	CTTGTAAGAA	AATGTGATGA	ATGGATTCCC	300
	GACCCACCGC	GTGCCATTGA	AAAACCGTTC	CTTATGGCCA	TTGAGCACGT	350
	TTTTGAGGTT	GGAAAGGATA	AGAAGGCCGT	TGTTGTGAGC	GGGCGTGTGG	400
	ACCAGGGGCA	GTTGAAGGTC	GGCGCAGATG	CAGAACTTTC	CGGGTTTAGC	450
	GCAAAGAAGC	TGACGGTGAA	GGTTGCTAGC	ATCGAAATGT	ACCATAAAAT	500
30	TCTGGAGGAT	TGCATGCCTG	GTGACTCTGT	TGGCGCGAAG	ATCGTTGGCA	550
	GCGGTGAAAC	AGTGAACCTG	TGGAAGGAAA	ATGTGGAACG	CGGCATGGTA	600
	CTCTCCGCAC	CAGGTGCAAC	GACACTGTTC	AACAAGGTCC	GCGCGCAGGT	650
	GTACGTGTTG	ACAAAGGAAG	AAGGCGGTCT	TCACACAGCC	TTTAGTCCTC	700
	ACTATCGTCC	GCAGCTTTTC	TTCCACTGTG	CTGATGTCAC	GGCAGATATT	750
35	AACTTCCCGG	AAAGCGAGAA	GCTTGCAGGG	GAGCTGAACA	AAAAGTATGG	800
	CCGTGATGCG	GCGGAACAGA	AGAAGAAGGA	GGCAGAACTG	AAAGAGTTTG	850
	AAAAGACGCT	TGTCTGCATG	CCTGGTGATA	ACCGCGAACT	CCTGCTCACC	900
	CTTGCCATATC	CAATGCCAAT	GGAAAAGGGA	CTCAAG		936

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

	CGGCATTCTT	GTGGTGGCAG	CTAACGACGG	ATGCATGCCG	CAGACGCGTG	50
	AGCACCTGCT	TATTTGTTTC	CAGATTGGCC	TTCCTGCTCT	TGTATGCTTT	100
60	ATCAATAAGT	GTGACATGAT	GCAAGGGCAG	GAGGAAATGA	TTGAGCTTGT	150

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCTTATG	GCCATTGAGC	350
5	ACGTTTTTGA	GGTTGGAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGACT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTCGAAG	GAAAATGTGG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAAC TTC	CCGGAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGATATG	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGA	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATTCCCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCCGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCT	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCCCT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

15	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
	CGTGTTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGTACG	GCCAGATGAA	200
	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTTGC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
20	AACATCTACC	GTTTCACCCA	GGCTGGTTCT	GAGGTGAGTG	CCCTTTTGGG	350
	GCGCATCCCG	TCCGCCGTCG	GTTACCAGCC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
25	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCAGAAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTCGT	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCCAG	CCCTTCCAGG	TGGCTGAGGT	800
30	ATTCACCGGC	AAGCCCGGAC	GTTTCGTCGA	GCTGCAGGAC	ACCATCAGCG	850
	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

55	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTTTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGTACGG	ACAAATGAAC	200
55	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCCG	AAGTGAGTGC	GCTGTTAGGA	350
	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTCG	ATTACATCAG	450
60	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TCACTGATCC	CGCTCCAGCT	500

	ACCACTTTCT	CGCACTTGGA	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
	GGAGTTGGGT	ATTTACCCTG	CGGTCGACCC	GCTTGACTCA	ACGTCACGTA	600
	TGCTGTCGGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
	GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
5	TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
	CCCGTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
	TTCACCGGCA	AGCCTGGGAG	GTTCGTTGAA	CTACAGGATA	CCATCAGCGG	850
	TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884

10

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

	TGGAAGTATG	TAATAATGTG	GCCAAAAAGC	ATGGCGGTTA	CTCTGTTTTT	50
	GCAGGTGTAG	GTGAAAGGAC	GAGGGAGGGT	AATGAATTGT	ACCATGAAAT	100
30	GATGGAGACA	GGTGTATATA	AGAAAAAGGC	ACTAGGTGGT	GGGAAGTTTG	150
	ATTTTCAGTG	ATCTAAAGCA	GCGCTGGTCT	ATGGACAAAT	GAACGAGCCA	200
	CCTGGGGCCC	GTGCTAGAGT	GGCACTAACT	GGATTAACAG	TCGCAGAATA	250
	TTTCCGTGAC	GAACAAGGAC	AAGACGTGTT	GTTGTTTATT	GATAATATTT	300
	ACCGATTTAC	TCAGGCAGGG	TCTGAGGTTT	CAGCCTTGCT	AGGCCGTATA	350
35	CCTTCAGCTG	TGGGATACCA	GCCTACATTG	GCAACAGATC	TTGGCTGTTT	400
	ACAAGAACGA	ATTACTACGA	CCAAATCTGG	TTCAATCACC	AGTGACAAG	450
	CTGTGTATGT	GCCAGCAGAT	GATATTACTG	ATCCAGCGCC	TGCCACAAC	500
	TTTACTCACT	TGGACGCTAC	TACTGTACTT	AGCAGGCCAA	TTGCTGAACT	550
	CGGTATTTAT	CCAGCGGTAG	ACCCGTTGGA	TTCAACAAGC	CGTATGCTAA	600
40	GCGCGAACAT	TGTGGGAAAT	GAACACTATA	GTGTAGCCCG	TTCCGTGCAG	650
	AAGATACTGC	AAGATTACAA	ATCGCTTCAG	GACATTATTG	CCATTTTGGG	700
	TATGGATGAA	CTGTCGGAAC	AAGACAAAAA	TATAGTAGCC	CGAGCAAGGA	750
	AGATGCAAAG	GTTCTTATCA	CAGCCATTCC	AAGTGGCGGA	AGTTTTTACT	800
	GGTAAACCGG	GAAGATTGTG	GGAATTGGAA	GATACAATTG	CCGGGGCACG	850
45	AGATATAATT	GCGGGTAATT	G			871

2) INFORMATION FOR SEQ ID NO: 859

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania guyanensis*

481

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

5	TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
	CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
	GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
	GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
	GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
10	CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
	ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
	TGCAAGGGCG	GCAAGATCGG	CCTGTTTCGG	GGTGCCGGTG	TGGGCAAGAC	400
	TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
	TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
15	TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
	GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
	GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
	GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
	GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
20	ACCAGCCGAC	GCTTGCGGAG	GATCTTGGA	TGCTGCAGGA	GCGCATTACG	800
	TCGACGATCA	AGGGATCGAT	TACGTCGTG	CAGGCTGTGT	ACGTGCTGTC	850
	GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
	CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
	GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
25	CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
	ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
	GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCCCT	1150
	GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
	ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
30	TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 860

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

50	CTCGGAGGGC	GTCCCGCCCG	TGCTGACGGC	GCTGGATGTG	ACGGAGGACC	50
	TTGGCCGCGA	TGAGCCGCTG	ACGCTGGAGA	TCGTGCAGCA	CCTGGACGCG	100
	AACACCGGCC	GCTGCATTGC	GATGCAGACG	ACGGACCTGC	TGAAGCTGAA	150
	GTCGAAGGTT	GTGTCGACCG	GCGGCAACAT	CTCTGTGCCG	GTGGGCCGTG	200
	AGACGCTGGG	CCGCATCTTC	AACGTGCTGG	GCGACGCGAT	CGACCAGCGC	250
55	GGCCCCGTGG	GTGAGAAGAT	GCGCATGGCG	ATCCACGCCG	AGGCCCCGAA	300
	GCTGGCGGAT	CAGGCCGCGG	AGGACACGAT	CCTGACGACC	GGCATCAAGG	350
	TGATCGACCT	GATTCTGCCC	TACTGCAAGG	GTGGCAAGAT	CGGCCTGTTT	400
	GGCGGCGCCG	GTGTGGGCAA	GACCGTGATC	ATCATGGAGC	TGATTAACAA	450
	CGTCGCGAAG	GGCCACGGTG	GTTTCTCGGT	GTTTGCCGCG	GTTGGCGAGC	500
60	GCACGCGCGA	GGGCACGGAC	CTGTACCTGG	AGATGATGCA	GTCGAAGGTG	550

	ATTGACCTGA	AGGGCGAGTC	GAAGTGCCTG	CTTGTGTACG	GGCAGATCAA	600
	CGAGCCCCCG	GGTGC GCGCG	CGCGCGTTGC	GCAGTCTGCG	CTGACGATGG	650
	CGGAGTACTT	CCGAGACGTG	GAGGGCCAGA	ATGTGCTGCT	GTTTCATCGAC	700
	AACATCTTCC	GCTTCACGCA	GGCGAACTCC	GAGGTCTCTG	CGCTGCTGGG	750
5	CCGCATTCCG	GCCGCCGTGG	GCTACCAGCC	GACGCTTGCG	GAGGATCTTG	800
	GTATGCTGCA	GGAGCGCATC	ACGTCGACGA	CGAAGGGGTC	GATCACGTCC	850
	GTGCAGGCCG	TGTACGTGCC	TGCGGATGAT	ATCACGGATC	CGGCGCCCGC	900
	GACGACGTTT	TCGCACCTGG	ACGCGACGAC	TGTGCTGGAC	CGCGCGGTGG	950
	CGGAGTCGGG	GATCTACCCT	GCCGTGAACC	CGCTGGAGTG	CGCGTCGCGT	1000
10	ATCATGGACC	CCGATGTGAT	CGACGTGGAC	CACTACAACG	TTGCGCAGGA	1050
	TATCGTGCAG	ATGCTGACCA	AGTACAAGGA	GCTGCAGGAT	ATCATTGCGG	1100
	TGCTTGGTAT	CGACGAGCTG	AGCGAGGAGG	ACAAGGTCGT	GGTGGACCGC	1150
	GCGCGCAAGG	TGACCCGTTT	CCTGTCGCAG	CCGTTCCAGG	TTGCGGAGGT	1200
	GTTTCACGGGC	ATGACGGGCC	AC			1222

2) INFORMATION FOR SEQ ID NO: 861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	CGATGAGCCG	50
35	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACCG	GCCGCTGCAT	100
	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	GTTGTGTCGA	150
	CCGGCGGCAA	CATCTCTGTG	CCGTTGGGCC	GTGAGACGCT	GGGCCGACATC	200
	TTCAACGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	TGGGCGAGAA	250
	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	GATCAGGCCG	300
40	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	CCTGATTCTG	350
	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	CCGGTGTGGG	400
	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	AAGGGCCACG	450
	GTGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	CGAGGGCACG	500
	GACCTGTACC	TGGAGATGAT	GCACTCGAAG	GTGATTGACC	TGAAGGGCGA	550
45	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	GAACGAGCCC	CCGGGTGCGC	600
	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	CTTCCGCGAC	650
	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	TCCGCTTCAC	700
	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	CCGGCCGCCG	750
	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
50	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
55	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	GGTGTTTACG	GGCATGACGG	1200
	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

2) INFORMATION FOR SEQ ID NO: 862

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
20	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTCTGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCGATC	TTCAAYGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
	TGGGCGAGAA	GATGCGCATG	CGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
25	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
30	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	850
35	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
40	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	GGTGTTTCACG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
	TGGCCTGCTG	ATGGG				1265

2) INFORMATION FOR SEQ ID NO: 863

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGGG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCGG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTC	GGCCGCAGAC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTCGC	GCCAGGTTGG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTCC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAACG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTCGC	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGGAGCG	CGCGGTCGAC	GGTGCGTTCC	TGATGCCGGT	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACGG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCAG	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTCGAG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCG	900
20	ATCAACCCGC	ACACGGACTT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCGATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCGG	TGCCGGCGTC	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Trypanosoma brucei*
- (B) STRAIN: LVH/75/USAMRU-K/18
- (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

45

	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTCGA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CAGTATTATT	GATGCTCCTG	GGCACCCTGA	CTTCATCAAG	300
	AACATGATCA	CCGTCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTTG	350
	CTCTGCGCAG	GGTGAGTTTC	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCAC'TTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCCGTGGTAT	TGGCACCGTG	750

CCC	TTG	GTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGTGAC	800
GTT	TGC	CCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
ACG	AGC	AGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
AAG	AAC	GT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CA	GAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
TC	CT	GAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
TG	CC	ACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
CG	AC	CGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
CT	GG	CGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	G	AGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
G	C	CCAGACC	GTCGCTGTCTG	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
G	T	TCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

A	A	G	C	T	C	A	A	G	G	T	A	T	A	C	C	A	T	C	G	A	T	T	A	T	G	50	
G	C	A	A	T	T	C	G	A	A	C	C	C	C	A	A	A	A	T	A	C	C	A	C	T	G	T	100
A	C	A	G	A	G	A	T	T	T	C	A	T	C	A	A	G	A	A	T	A	T	G	T	G	T	T	150
G	C	T	T	T	A	T	T	G	G	T	T	G	T	C	C	C	A	G	C	T	T	T	C	A	G	G	200
35	A	G	G	T	C	A	A	A	C	C	A	G	A	A	C	A	T	G	C	T	T	T	A	T	T	G	250
A	A	A	T	G	A	T	T	G	T	C	G	G	T	A	T	T	A	A	C	A	A	G	A	T	G	A	300
C	G	T	T	T	T	G	A	T	G	A	A	A	T	C	T	T	C	A	A	C	G	A	A	T	T	G	350
T	T	A	C	A	A	C	A	C	C	G	A	A	G	A	T	C	C	C	A	T	T	C	G	T	T	G	400
A	T	A	A	T	A	T	G	G	T	T	G	A	G	A	G	A	T	C	T	C	A	A	G	A	T	G	450
40	T	T	A	G	T	C	G	A	A	G	C	C	C	T	C	G	A	C	A	C	A	T	T	A	C	A	500
G	C	C	A	C	T	C	C	G	T	C	T	C	C	A	T	T	A	C	A	A	G	A	T	G	T	T	550
C	T	G	T	C	C	C	A	G	T	C	G	T	G	T	T	G	A	G	A	C	T	G	G	T	A	C	600
G	T	T	A	C	C	T	T	C	G	C	T	T	C	G	T	G	G	A	A	G	T	T	A	A	G	T	650
G	C	A	C	C	A	T	G	A	G	C	A	G	C	C	A	G	A	G	C	C	T	C	C	C	A	A	700
45	A	T	G	T	T	A	A	G	A	A	C	G	T	C	C	A	T	C	A	T	C	A	T	C	A	T	750
G	A	T	G	C	C	A	A	G	A	C	A	G	A	C	C	A	G	C	A	G	C	T	T	C	A	A	800
T	A	T	C	G	T	C	C	T	C	A	A	C	C	C	A	G	A	A	T	C	A	A	G	A	A	T	850
T	T	G	A	C	T	G	T	C	A	C	A	C	C	G	T	C	A	C	A	C	A	T	T	C	G	A	900
A	A	G	A	T	G	G	A	C	A	C	A	G	A	T	C	T	G	G	A	A	A	A	A	C	C	A	950
50	C	A	A	G	T	C	T	G	G	T	G	A	T	G	C	T	T	T	G	A	A	C	C	T	T	T	1000
G	T	G	T	T	G	A	G	G	C	C	T	T	C	A	C	T	G	A	C	T	T	C	A	C	T	T	1050
G	A																								1052		

2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGCGCAT	100
GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15 TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
TGCATTCGAT	CAATTATCAA	CAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20 TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
TGCGCGTATG	CGTGTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25 GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zoogloea ramigera*
(B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

AAGGTATTCTG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50 CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
ATGGTGCCAG	TCGGTAAAGC	AACCTGGGT	CGCATCATGG	ACGTGCTGGG	200
TAACCCGATC	GACGAATGCG	GCGCGTCCG	TCACGACCAG	ATCGCTTCGA	250
TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTCGCCATC	GCAAGATCTG	300
CTGGAAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCGT	TCGCCAAGGG	350
55 CGGTAAAGTC	GGTCTGTTTC	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
TGATGGAAC	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60 GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	C C G C T T C A C C	CTGG C C C G G T A	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
25 CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
30 CACCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
35 TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	700
TACTACTGAC	GTAACGGTG	TTGTTAACCT	ACCAGAAGGT	ACTGAAATGG	750
40 TTATGCCTGG	CGATAACGTT	GAAATGGA			778

2) INFORMATION FOR SEQ ID NO: 869

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
60 GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

488

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACT	TATTGTGAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAAACTGCT	AAAACAACTG	TAAGTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTG	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

30	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTGAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACCTGTA	ACTGGTGTG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTGTC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTTAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTT	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACGTGTA	CTGGTGTGTA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AACTGCTAA	AACAACGTGA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

55

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

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GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT      150
10 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA      200
GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGATACT GACAAACCAT      300
TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA      400
15 AATCGTTGGT ATTGCTGACG AAACCTGCTAA AACAACTGTA ACAGGTGTTG      450
AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT      600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC AACTCCATT C                641
20

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2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: LSPQ 2514

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

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ACCAGCATTG TAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
40 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG      200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC      250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
45 TACAGGCCGT GTTGAACGTG GGCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG      400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
CTCCAGGTTC AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
50 TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG      600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACCTAC      650
CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A                681

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55

2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: R591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTTC	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCGT	ACTACTGACG	650
25	TAAGTGGTGT	TGTAAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAATCC	250
50	AGAACGTGAT	TCTGACAAAC	CATTTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAACTGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTGTC	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTAAGTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
20	ATCTTATTAT	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
	GTAATCGCTG	TTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	250
	ACAAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	300
25	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
	AAACAACGTG	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTG	CACGTGAAGA	550
30	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
	TGACGTAACT	GGTGTTGTAA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
35	CTGGCGACAA	CGTTGAAATG				770

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

	TTGTATTCTT	AAACAAAGTT	GACATGGTAG	ACGACGAAGA	ATTATTAGAA	50
55	TTAGTTGAAA	TGGAAGTTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	100
	TGACGATGTA	CCTGTAATCG	CTGGTTCTGC	ATTAAAAGCA	TTAGAAGGCG	150
	ATGCTGAATA	CGAACAAAAA	ATCTTAGACT	TAATGCAAGC	AGTTGATGAT	200
	TACATTCCAA	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	250
	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	300
60	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	CATCGGTATG	350

	CACGAAACTT	CTAAAACAAC	TGTTACTGGT	GTAGAAATGT	TCCGTAAATT	400
	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	TTACGTGGTG	450
	TTGCACGTGA	AGACGTACAA	CGTGGTCAAG	TATTAGCTGC	TCCTGGTTCT	500
	ATTACACCAC	ACACAAAATT	CAAAGCTGAA	GTATACGTAT	TATCTAAAGA	550
5	TGAAGGTGGA	CGTCACACTC	CATTCTTCAC	TAACTATCGC	CCACAATTCT	600
	ATTTCCGTAC	TACTGACGTA	ACTGGTGTG	TAACTTACC	AGAAGGTACA	650
	GAAATGGTTA	TGCCTGGCGA	CAACGTTGAA	ATGACAGTTG	AATTAATCGC	700
	TCCAATCGCT	ATCGAA				716

10

2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
30	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCCGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
40	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

2) INFORMATION FOR SEQ ID NO: 880

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60	CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCATG	CCGCAGACCC	50
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	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCCTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAC TGGT	150
	CGAGATGGAA	GTTCGCGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAAGAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTAC	GTGCTGTCCA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTTGAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

495

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCAGAA	150
	TACGATTTC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAACTCCAG	AACGTGATAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGTGAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACTGT	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

55

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTCAT	300
GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
AAACCACTGA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

2) INFORMATION FOR SEQ ID NO: 885

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTCCT	50
TACATCGTTG	TATTCTTGAA	CAAAGTAGAC	ATGGTTGATG	ACGAAGAATT	100
ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
TCCCTGGTGA	CGATGTTTCT	GTAGTTGCTG	GATCAGCTTT	GAAAGCTCTA	200
GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250
TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTTCATGA	300
TGCCAGTTGA	AGACGTGTTC	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAGTTGT	400
TGGTATTGCT	GAAGAAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

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CGGCCCAATG CCTCAAATC GTGAACACAT CCTATTGTCT CGTCAAGTTG      50
GTGTTTCCTTA CATCGTTGTA TTCCTTGAACA AAGTAGACAT GGTTGATGAC      100
GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA      150
ATACGAATTC CCTGGTGACG ATGTTCTCTGT AGTTGCTGGA TCAGCTTTGA      200
AAGCTCTAGA AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG      250
GCTGCAGTTG ACGAATACAT CCAACTCCA GAACGTGACA ACGACAAACC      300
ATTCATGATG CCAGTTGAAG ACGTGTCTC AATTACTGGA CGTGGTACTG      350
TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT      400
GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT      450
TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCTGGA GACAACATTG      500
GTGCTTTACT ACGTGGTGT GCACGTGAAG ACATCCAACG TGGACAAGTT      550
TTAGCTAAAC CAGGTACAAT CACACCTCAT ACAAATTCT CTGCAGAAGT      600
ATACGTGTTG ACAAAGAAG AAGGTGGACG TCATACTCCA      640

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2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

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ATCCTGGTTT GCTCCGCAGC TGACGGCCCA ATGCCACAGA CCCGCGAGCA      50
CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCTCTGA      100
ACAAGTGC GA CCGTGGTGAC GACGAGAAC TGCTGGAAC TGTGCGAAATG      150
GAAGTGC GTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC      200
AATCATCAAG GGTTCGGCAC GTATGGCGCT GGAAGGCAAA GAAGGCGAGA      250
TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC      300
CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA      350
CGTGTCTCTG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC      400
GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC      450
ACCGTCAAAA CCACTTGCAC CGGCGTGGAA ATGTTCCGCA AGCTGCTGGA      500
CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC      550
GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG      600
CCGCACAACC ACTTCACCGG CGAGATCTAC GTTCTGTCGA AAGATGAAG      650

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CGGCCGTCAC	ACCCCGTTCT	TCAACAACATA	TCGTCCACAG	TTCTACTTCC	- 700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

5

2) INFORMATION FOR SEQ ID NO: 888

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 634 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecalis*
 - (B) STRAIN: R503
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

25	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
	TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCCA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
30	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

40 2) INFORMATION FOR SEQ ID NO: 889

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus fumigatus*
 - (B) STRAIN: ATCC 14110
- 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55	TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
	TTCGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
	GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTACTCGTGA	150
	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTCAGCTCG	200
60	AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTCG	GACAGATGAA	CGAGCCCCCC	250

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTGCGTG	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTTCAGC	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCTGT	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
35	TTCCATCACC	TCCGTC				466

2) INFORMATION FOR SEQ ID NO: 891

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCTG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTC	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTCGCCGA	GTAATTCCGT	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTCGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

5

2) INFORMATION FOR SEQ ID NO: 892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 481 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
25 TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTTCAT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCCGG	TGCCCCGTGCC	250
CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
30 CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCGGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

35

2) INFORMATION FOR SEQ ID NO: 893

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1208 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 14285

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
55 GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTTGGCA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
60 AGACCTCTGT	CATTACGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTT	450

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCCGTGTCG	CCTTGACCGG	500
	TTTGAAGTGC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCTTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCGA	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGAACT	TATTGTAAGC	CGCCCTCTTT	ATGCATTGAG	GGTGAATAAG	50
	AAGGCTGACA	GGTAATAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	100
	CGTGTTCACT	GGTGTGCGTG	AGCGTACCCG	TGAAGGAAAC	GATCTGTACC	150
	ATGAAATGCA	GGAACCCCGC	GTCATCCAGC	TTGATGGCGA	GTCTAAGGTC	200
40	GCCCTTGTTG	TCGGTCAGAT	GAACGAGCCC	CCTGGAGCCC	GTGCCCCTGT	250
	CGTCTTTACT	GGTCTTACCG	TTGCCGAATA	CTTCCGTGAC	GAGGAGGGCC	300
	AAGATGGTAC	GCCTTTTTTAC	TCTTCTTATT	CTTCGGGTCG	GACTACAGAA	350
	CTAACCTGCT	CCAGTGCTTC	TCTTCATTGA	TAACATTTTC	CGTTTCACAC	400
	AAGCCGGTTC	TGAGGTGTCT	GCCTTGCTTG	GACGTATTCC	CTCTGCCGTC	450
45	GGTTACCAGC	CCACTCTCGC	CGTCGACATG	GGTGGTATGC	AGGAACGTAT	500
	CACAACCACC	AACAAGGGTT	CCATTACTTC	CGTG		534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

5 CAAGGCTCAC GGTGGTACT CCGTCTTCAC TGGTGTCCGGT GAGCGTACCC 50
 GTGAGGGTAA CGATCTGTAC CACGAAATGC AGGAGACCTC GGTCATTCAG 100
 CTCGAGGGCG AGTCTAAGGT GGCCCTGGTC TTTGGTCAGA TGAACGAGCC 150
 CCCGGGTGCT CGTGCCCGTG TCGCTCTTAC TGGTCTTACC GTCGCCGAGT 200
 10 ACTTCCGTGA CCAGGAGGGT CAGGATGGTT AGTTCTCGTC CACTCATGCC 250
 GAAACATGTG CGTGTTCCGA GGCTAATCAA CGTGCCAGTG CTGCTTTTCA 300
 TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCCGAGGT GTCTGCCCTG 350
 CTGGGTCGTA TCCCCTCTGC CGTCGGTTAC CAGCCCACCC TCGCCGTCGA 400
 15 CATGGGTGGC ATGCAGGAGC GTATCACCAC CACCAAGAAG GGCTCTAT 448

2) INFORMATION FOR SEQ ID NO: 896

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*
 30 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

ATTCAGGAGC TGATTGTAAG TTGCCAATCC ATGAACTGGA GATTTGGTGT 50
 35 GACCCATAGA ACTAACAAAT TATTTAGAAC AACATCGCCA AGGCTCACGG 100
 TGGTTACTCC GTCTTCTGTG GTGTCGGTGA GCGTACTCGT GAGGGTAACG 150
 ATCTGTACCA CGAAATGCAG GAGACTGGTG TCATCCAGCT CGAGGGTGAC 200
 TCCAAGGTCG CTCTGGTCTT CGGTGAGATG AACGAGCCCC CGGGTGCCCCG 250
 TGCCCGTGTC GCCCTTACCG GTCTGACCAT TGCCGAGTAC TTCCGTGACG 300
 40 AGGAGGGTCA GGACGTGCTG CTCTTCATTG ACAACATTTT CCGTTTCACC 350
 CAGGCCGGTT CTGAGGTGTC TGCCCTTCTG GGTCGTATCC CCTCTGCCGT 400
 CGGTTACCAG CCCACTCTGG CCGTCGACAT GGGTGGTATG CAGGAGCGTA 450
 TTACCACCAC CACCAAGGGT TCCATTACCT CCG 483

2) INFORMATION FOR SEQ ID NO: 897

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 60 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTTCGGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCC	CCGTCTCTCGA	950
	CTGCCACACT	GCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Penicillium marneffe*
 (D) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCCTCTGG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTC	GTTCTTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCCTGG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTACACT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCCTT	1200
	CCAAGCCCAT	GTGTGTTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCGCCGTTT	GCGAGTAAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

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2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1147 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Piedraia hortai*

(B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTTC	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAAGTGGCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCGGTGGTAT	CGGAAGTGT	650
45	CCTGTGCGCC	GTATCGAGAC	TGGTGTCTC	AAGCCCGGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCCGCTTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCCACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
55	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

(i) SEQUENCE CHARACTERISTICS:

505

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

15	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
	CGAGACTGGT	CGCAATTTCC	ACGTCGCTAA	CGTGCTTGAA	CAGACGCTCC	150
	CGGCCACCGT	GACTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCTG	200
	ACTGCGCTAT	CCTCATTATC	GCTGCCGGCA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
20	CGGTGTAAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
	GGTCTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
	TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
25	CTTGAGGCCA	TCGACTCCAT	CGAGCCCCCC	AAGCGCCCCA	GCGACAAGCC	600
	CCTCCGCCTT	CCCCTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
	TCCCTGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	CATGGTCGTG	700
	ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
	CCACGAGCAG	CTCTCCGAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
30	TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
	TCCAAGAACG	ACCCCCCTCT	GGGTGCCGCT	TCTTTCGATG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGGTCGGTGC	TGGCTACGCC	CCCGTCCTCG	950
	ACTGCCACAC	CGCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
	ATCGACCGCC	GTACCGGCAA	GTCTGTGCGAG	TCCGCCCCCA	AGTTCATCAA	1050
35	GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
	TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32075

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

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	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTTCGTT	100
	CCCATTCTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
60	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCTCTCA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTGCG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCGG	CATGGTCGTC	ACCTTTGCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

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2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
GATTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
15 TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCT	CGGTGTCCGT	250
CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
20 CGGATACAAC	CCTAAGAACG	TTCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCTGGTA	CAAGGGTTGG	500
GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCCT	600
CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTCAC	650
25 AGCCCCCTCCG	TCTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
ACGGTTCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
TGCTAACTTG	ACACTCAGCG	CTCCCGCCAA	CGTCACCACT	GAAGTCAAGA	850
GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
30 GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCGTGGTAA	950
CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
ACGCCCAGGT	CATCGTCCTC	AACCACCCCCG	GTCAGGTCGG	TGCTGGTTAC	1050
GCCCCAGTCC	TCGATTGCCA	CACTGCCCAC	ATTGCTTGCA	AGTTCGCTGA	1100
GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
35 CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1200
AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCCTCCTC	TCGGTCGTTT	1250
CGCCGTTCGC	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
TTCTCCTCCG	TCTTCCATAT	ATATTTTTC	AGTTATATGT	GACTAACCAC	1350
AAATCACGGG	AATAGC				1366

2) INFORMATION FOR SEQ ID NO: 904

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GACTCGTGAG	50
60 CATCTGCTGC	TCGCCCGCCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCTGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTACTGGCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCG	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 967 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Aspergillus niger*

(B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCGG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTCAT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800
	ATTCCGTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCGCCGTA	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
55	CCGGTCAGCG	CTTCAAC				967

2) INFORMATION FOR SEQ ID NO: 906

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(i) SEQUENCE CHARACTERISTICS:

509

(A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

15	TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
	CCCGACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
20	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCTGT	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
25	GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTAAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
	CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCCGGTGAC	AACGTCGAGA	800
30	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

55	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCGTCAGG	TCGGTGTCCA	150
	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCCTGAGA	200
55	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TTGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
	TTCCTCATGT	CTGTCGAGGA	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
60	TGCCTCCGGC	CGTGTCGAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500

510

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTCTG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTGCTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTCAAGAA	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAATCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCCG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTTC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCGGA	600
	CAAGTCAAGG	CTCACAAGAA	GTTCTTGTG	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAAA	700
	TGTTTCATCC	AACTGCCGAT	GAATCCTGCG	CACTTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

50 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

5
 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 10 TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 15 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 TGCATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 20 GAAGGTGGTC GTCGTAATGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850
 CAGTCCAAGC AGGTCATGCC CCGTGACAAC GTTGAGATGA TCTTGAAGAC 900
 ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931
 25

2) INFORMATION FOR SEQ ID NO: 910

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

40 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 45 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 50 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 TGCATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 GAAGGTGGTC GTCGTAATGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 60 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850

CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

35

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

GACGGYSYCA TGCKKCAGAC

20

50

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

5

GAARAGCTGC GGRCGRTAGT G

21

10 2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

25

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

40

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

55

2) INFORMATION FOR SEQ ID NO: 918

60 (i) SEQUENCE CHARACTERISTICS:

514

- (A) LENGTH: 1391 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

15	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGAAACCAT	CTCTACCGGT	TCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTT	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTCTGCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTAA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCGART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

TARAA YTTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

5 2) INFORMATION FOR SEQ ID NO: 924

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20 2) INFORMATION FOR SEQ ID NO: 925

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35 2) INFORMATION FOR SEQ ID NO: 926

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50 2) INFORMATION FOR SEQ ID NO: 927

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATTA	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
45 TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCC GTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCC GGAC	CGGATGCATT	CCCGATGGAC	350
CTGTCCTCAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
50 GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

2) INFORMATION FOR SEQ ID NO: 930

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides distasonis*

5 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

	GCTATCTCTA	AACAAGCGGA	AGCGGATATC	GTGATTATCG	CCGCCTGCGG	50
10	TGAGCGTGCG	AATGAGGTCG	TAGAGGTATT	TACGGAGTTC	CCGGAATTGG	100
	TAGACCCGCA	TACGGGACGT	AAATTGATGG	AACGTACGAT	CATTATCGCC	150
	AATACATCCA	ACATGCCGGT	AGCCGCTCGT	GAGGCATCCG	TATATACGGC	200
	GATGACCATC	GCCGAGTATT	ATCGCAGCAT	GGGTTTGAAG	GTTCTGTTGA	250
	TGGCCGACTC	TACTTCCCGC	TGGGCACAGG	CTTTGCGTGA	GATGTCCAAC	300
15	CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
	TATCGTGGCG	AACTTCTACG	CTCGTGCGGG	ATTCGTTTCAT	TTGAATAACA	400
	ACGCTACAGG	CTCCGTCACT	TTCATCGGTA	CGGTATCG		438

20

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 453 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas asaccharolytica*

(B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

	CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
	CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
	CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
40	CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCGG	200
	TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
	GTACTCCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
	GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
	ACTTGTCGGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
45	CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
	AGC					453

50 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
 TTCATGAACA AATGTGACAT GGTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA ATTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
 10 ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
 GACTGGGAAG CTAAGATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA 400
 CGTGGAACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
 15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTT CGTAAATTAC 500
 TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGTG 550
 GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACGCCCC ACAATTCTAT 700
 20 TTCCGTACTA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
 AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
 CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

60

520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

2) INFORMATION FOR SEQ ID NO: 937

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATACIGARG YITTYGGIGA RTT

23

2) INFORMATION FOR SEQ ID NO: 938

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: D10023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

ATGTCTCAAG	TTCAAGAACA	ACATATATCA	GAGTCACAGC	TTCAGTACGG	50
GAACGGTTTCG	TTGATGTCCA	CTGTACCAGC	AGACCTTTCA	CAGTCAGTCG	100
TTGATGGAAA	CGGCAACGGT	AGCAGCGAAG	ATATTGAGGC	CACCAACGGC	150
TCCGGCGATG	GTGGCGGATT	GCAGGAGCAA	GCGGAAGCGC	AAGGTGAAAT	200
GGAGGATGAA	GCATACGATG	AAGCTGCCTT	AGGTTTCGTTT	GTGCCAATAG	250
AAAAACTGCA	AGTGAACGGG	ATTACTATGG	CGGATGTGAA	AAAACATAAGG	300
GAGAGTGGGC	TTCACTGCTG	TGAAGCGGTA	GCATATGCTC	CCAGAAAGGA	350
TTTATTGGAA	ATCAAAGGTA	TATCGGAAGC	TAAGGCAGAT	AAGTTGCTAA	400
ACGAAGCGGC	AAGGCTAGTG	CCTATGGGAT	TTGTCACGGC	TGCTGATTTT	450
CATATGAGAA	GATCGGAGCT	GATTTGTTTG	ACAACGGGTT	CTAAGAATTT	500
GGACACTCTT	TTGGGTGGTG	GTGTGGAAAC	TGGTTCTATT	ACTGAGCTTT	550
TCGGTGAATT	CAGGACAGGT	AAGTCCCAGC	TATGTCACAC	TTTGGCCGTG	600
ACATGCCAAA	TTCCATTGGA	TATTGGTGGC	GGTGAAGGTA	AGTGTTTGTA	650
TATCGATACC	GAAGGTACTT	TCAGGCCCGT	AAGATTGGTA	TCCATAGCTC	700
AGCGGTTTCG	ATTAGACCCG	GATGATGCTT	TGAACAACGT	TGCGTATGCA	750
AGAGCCTATA	ACGCCGATCA	TCAGTTAAGA	CTTCTGGATG	CTGCTGCCCA	800
AATGATGAGC	GAGTCTCGGT	TTTCCTTGAT	TGTGGTCGAT	TCTGTTATGG	850
CTCTATACCG	TACGGATTTT	TCTGGTCGTG	GTGAACTAAG	CGCAAGGCAA	900
ATGCATTTAG	CCAAATTTAT	GCGTGCTTTG	CAAAGGCTGG	CCGACCAATT	950
TGGTGTGCA	GTCGTCGTTA	CTAACCAAGT	GGTCGCCCAA	GTTGATGGTG	1000
GTATGGCTTT	TAATCCAGAT	CCAAAGAAGC	CTATCGGTGG	TAATATTATG	1050
GCACATTCTT	CCACCACGCG	ATTAGGTTTC	AAAAAGGGTA	AGGGATGTCA	1100
AAGATTATGC	AAAGTTGTTG	ACTCACCTTG	CTTACCAGAG	GCTGAATGTG	1150
TGTTTCGCGAT	CTATGAAGAT	GGTGTTGGTG	ACCCAGAGA	AGAAGACGAG	1200
TAG					1203

2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: GRF88
 (C) ACCESSION NUMBER: M87549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA\	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAAACCT	CTGCTGTAGA	GGTTCTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATAC	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
30	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus humicola*
 (B) STRAIN: ATCC 38294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

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CGTCCTTATC CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT      50
TCTCCGTCCT CACCGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGACCTG      100
TACCACGAGA TCGGTGAGAC TGGTGTTCATC AACCTCGAGG GCGACTCCAA      150
GGTCGCTCTC GTCTTCGGCC AGATGAACGA GCCCCCCGGA GCCCGTGCCC      200
GTGTGCGCCCT TACCGGCCCTC ACCATCGCCG AGTACTTCCG TGACGAGGAG      250
GGTCAGGACG TGCTTCTCTT CATCGACAAC ATTTTCCGTT TCACCCAGGC      300
CGGTTCCGAG GTGTCTGCCC TTCTCGGTCTG TATCCCCTCG GCCGTGCGTT      350
ACCAGCCCAC CCTCGCTACC GACATGGGTT CCATGCAGGA GCGTATCACC      400
ACCACCAAGA AGGGTTCGAT TACCTCCGTC                                430

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2) INFORMATION FOR SEQ ID NO: 942

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

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CGTGTACGAT GCTCTTGAGG TGCAAAATGG TAATGAGCGT CTGGTGCTGG      50
AAGTTCAGCA GCAGCTCGGC GGCGGTATCG TCGGTACCAT CGCAATGGGT      100
TCCTCCGACG GTCTGCGTCG CGGTCTGGAT GTAAAAGACC TCGAACACCC      150
GATCGAAGTC CCGGTAGGTA AAGCGACTCT GGGCCGTATC ATGAACGTAC      200
TGGGTGAACC GGTCGACATG AAAGGCGAGA TCGGTGAAGA AGAGCGTTGG      250
GCGATTACAC GCGCAGCACC TTCCTACGAA GAGCTGTCAA ACTCTCAGGA      300
ACTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT CCGTTCGCTA      350
AGGGCGGTAA AGTTGGTCTG TTCGGTGGTG CGGGTGTAGG TAAAACCGTA      400
AACATGATGG AGCTCATTCG TAACATCGCG ATCGAGCACT CCGGTTACTC      450
TGTGTTTGCG GGCGTAGGTG AACGTACTCG TGAGGGGAAC GACTTCTACC      500
ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT GGTGTATGGC      550
CAGATGAACG AGCCGCCGGG AAACCGTCTG CGCGTAGCTC TGACCGGTCT      600
GACCATGGCT GAGAAATTCC GTGACGAAGG TCGTGACGTT CTGCTGTTCTG      650
TTGACAACAT CTATCGTTAC ACCCTGGCCG GTACGGAAGT ATCCGCACTG      700
CTGGGCCGTA TGCCTTCAGC GGTAGGTTAT CAGCCGACCC TGGCGGAAGA      750
GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAACCC GGTT              794

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2) INFORMATION FOR SEQ ID NO: 943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTACGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATTGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
25	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCGGTG	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
30	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
35	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACTGGTTCTA	TCAC				814

2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55	GTGTACGATG	CTCTTGAGGT	GCAAAATGGT	AATGAGCGTC	TGGTGCTGGA	50
	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	GCGTACCATC	GCAATGGGTT	100
	CCTCCGACGG	TCTGCGTCGC	GGTCTGGATG	TAAAAGACCT	CGAACACCCG	150
	ATCGAAGTCC	CGGTAGGTAA	AGCGACTCTG	GGCCGTATCA	TGAACGTACT	200
60	GGGTGAACCG	GTGACATGA	AAGGCGAGAT	CGGTGAAGAA	GAGCGTTGGG	250

	CGATTACACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTC	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTGCGGTG	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

50 2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

	GCGACGCTAT	CCCGCATGTT	TACGATGCCC	TGAAATTGGA	CGAGAACGGT	50
	CTGACTCTGG	AAGTTCAACA	ACTTCTGGGT	GACGGCGTTG	TCCGTACTAT	100
	TGCAATGGGT	AGTTCAGACG	GCCTGAAACG	CGGCATGTCT	GTAAGCAATA	150
10	CTGGTGCGCC	AATCACTGTG	CCGGTAGGTA	AAGGTACTTT	GGGTCGTATT	200
	GTCGACGTAT	TGGGTACGCC	TGTTGATGAA	GCAGGTCCGA	TCGATAACCGA	250
	CAAGAGCCGT	GCCATTCCACC	AAACTGCTCC	GAAATTTCGAC	GAGTTGTCTG	300
	CAACTACCGA	ATTGTTGGAA	ACCGGTATTA	AAGTGATCGA	CTTGCTGTGT	350
	CCGTTTGCTA	AAGGCGGTAA	AGTAGGTCTG	TTCGGTGGTG	CCGGTGTAGG	400
15	CAAAACCGTG	AACATGATGG	AATTGATCAA	CAACATCGCC	AAAGCGCACA	450
	GCGGTCTGTC	CGTGTTCGCA	GGTGTGGGCG	AGCGTACCCG	TGAAGGTAAC	500
	GACTTCTACC	ACGAGATGAA	AGATTCCAAC	GTATTGGATA	AAGTGGAAT	550
	GGTTTACGGT	CAGATGAACG	AACCTCCGGG	CAACCGTTTG	CGCGTCGCAT	600
	TGACCGGTTT	GACCATGGCG	GAATACTTCC	GTGACGAAAA	AGACGAAAC	650
20	GGTAAAGGTC	GCGACGTATT	GTTCTTCGTT	GACAACATCT	ACCGTTACAC	700
	TCTGGCCGGT	ACCGAAGTAT	CTGCACTGTT	GGGCCGTATG	CCTTCTGCAG	750
	TGGGTTACCA	ACCGACATTG	GCTGAAGAAA	TGGGTCGTTT	GCAAGAGCGT	800
	ATTACCTCTA	CCCAAACCGG	TTCCATTACT	TC		832

25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

	TCCGCGCGAT	GCCATTCCGC	ATGTTTACGA	CGCCCTGAAA	TTGGATGCAA	50
	ACGGCCTGAC	TTTGGAAGTA	CAACAGCTTC	TGGGCGACGG	CGTGGTTTCGT	100
45	ACTATTGCAA	TGGGTAGTTC	GGACGGTCTG	AAACGCGGCA	TGACTGTAAG	150
	CAATACAGAT	GCGCCGATTA	CTGTGCCGGT	AGGTAAAGGT	ACTTTGGGAC	200
	GTATTGTGCA	TGTGTTGGGT	ACACCTGTTG	ATGAAGCAGG	TCCGATTGAT	250
	ACCGACAAAC	ACCGTGCTAT	CCATCAGACA	GCTCCGAAAT	TCGATGAGTT	300
	GTCTGCTACT	ACCGAGCTGC	TGGAAACAGG	CATTAAAGTG	ATTGACTTGC	350
50	TGTGTCCGTT	TGCCAAAGGC	GGTAAAGTAG	GTCTGTTTCGG	TGGTGCCGGT	400
	GTAGGCAAAA	CCGTCAACAT	GATGGAATTG	ATTAACAACA	TCGCCAAAGC	450
	GCATAGTGGT	TTGTCCGTGT	TCGCCGGTGT	GGGGGAACGT	ACCCGTGAAG	500
	GTAACGACTT	CTACCACGAG	ATGAAAGATT	CCAACGTATT	GGACAAAGTG	550
	GCGATGGTTT	ACGGTCAGAT	GAACGAACCT	CCGGGTAAAC	GTCTGCGTGT	600
55	AGCCTTGACC	GGTTTGACGA	TGGCCGAATA	CTTCCGTGAT	GAAAAAGACG	650
	AAAGCGGCAA	AGGTCGCGAC	GTATTGTTCT	TCGTGGACAA	CATTTACCGT	700
	TACACTCTGG	CCGGTACAGA	AGTATCCGCA	TTGCTCGGTC	GTATGCCTTC	750
	AGCAGTAGGT	TACCAACCGA	CATTGGCTGA	AGAAATGGGT	CGTCTGCAAG	800
60	AGCGTATTAC	CCTCTACTCA	AACAGGCTCC	ATTACTTCTA		840

2) INFORMATION FOR SEQ ID NO: 948

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

	GCAGCTGGCG	ACAAGCTACC	TGAGATCAAT	AATGCACTTG	TAGTCTATAA	50
20	AAATGACGAA	AAAAAATCAA	AAATCGTCCT	TGAAGTAGCT	CTTGAGCTTG	100
	GTGATGGAGT	GGTTCGGACC	ATCGCTATGG	AATCAACGGA	TGGGTTGACT	150
	CGTGGCATGG	AAGTGCTAGA	TACTGGCCGT	CCAATTTCTG	TGCCAGTCGG	200
	CAAAGAAACA	CTTGGTTCGCG	TCTTTAACGT	TTTGGGAGAT	ACCATTGACT	250
	TGGATGCTCC	TTTTGCGGAT	GATGCAGAGC	GCCAGCCAAT	CCATAAGAAA	300
25	GCTCCAACCT	TTGATGAGTT	GTCTACTTCT	TCAGAGATCT	TAGAGACAGG	350
	TATCAAGGTT	ATCGACCTGT	TAGCCCCTTA	TCTGAAAGGT	GGTAAAGTTG	400
	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAGA	CCGTCCTGAT	TCAAGAATTG	450
	ATCCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCTGTAT	TTACTGGCGT	500
	TGGGGAACGT	ACCCGTGAAG	GGAATGACCT	TTATTGGGAA	ATGAAAGAGT	550
30	CTGGTGTTAT	CGAGAAAACA	GCCATGGTCT	TCGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCGC	GTATGCGGGT	TGCTTTGACT	GGTTTGACGA	TTGCAGAATA	650
	CTTCCGTGAT	GTGGAAGGTC	AAGATGTCTT	GCTCTTCATT	GACAACATCT	700
	TCCGTTTCAC	GCAGGCAGGT	TCTGAAGTTT	CTGCCCTTTT	GGGTCGGATG	750
	CCGTCAGCCG	TTGGTTACCA	ACCAACACTT	GCGACAGAAA	TGGGGCAATT	800
35	GCAAGAGCGT	ATCACATCGA	CTAAGAAGGG	TTCTGTAACC	TCT	843

2) INFORMATION FOR SEQ ID NO: 949

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GAGATGGTAT	GGTCCGTACT	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAATGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GATGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAACTT	TTGATGAATT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAGGTTG	400
	GACTTTTTCG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCAGTAT	TTACCGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GTAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGTGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTAACT	GGTTTGACAA	TCGCCGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAGCGT	ATTACATCAA	CTAAAAAGGG	TTCTGTAACC	T	841

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTGTAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	GTAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT	150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAAA	GAAACACTTG	200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT	250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA	300
	TGAGTTGTCT	ACCTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG	350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT	400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTGAG	GAATTGATCC	ACAACATTGC	450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC	500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG	550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT	600
	GCGGGTTGCT	TTGACTGGTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG	650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG	700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG	750
	TTACCAACCA	ACACTTGCGA	CTGAAATGGG	ACAACCTCAA	GAGCGTATTA	800
	CATCGACTAA	GAAAGGTTCT	GTAACCTT			827

50 2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

	GCAGCAGGGG	AAACACTTCC	TGAGATTAAT	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GTGATGGTAT	GGTCCGTACG	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
10	CGTGGAATGG	AAGTTTTGGA	CACAGGCCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACTATTGACT	250
	TGGATGCTCC	TTTCGCTGAA	GACGCTGAGC	GTCAGCCAAT	TCATAAGAAA	300
	GCTCCAACCT	TTGATGAATT	GTCTACCTCA	TCTGAAATCT	TGGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGGAAAGTTG	400
15	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTGAT	CCAAGAGTTG	450
	ATTCACAACA	TTGCCCAAGA	ACATGGTGGT	ATTTTCAGTAT	TTACCGGTGT	500
	TGGAGAACGT	ACCCGTGAGG	GGAACGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCA	600
	CCTGGAGCAC	GTATGCGTGT	TGCTCTTACT	GGTTTGACAA	TCGCCGAATA	650
20	CTTCCGTGAT	GTAGAAGGCC	AAGATGTGCT	TCTCTTTATC	GACAATATCT	700
	TCCGTTTCAC	TCAAGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGGATG	750
	CCTTCAGCCG	TTGGTTACCA	ACCAAACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CTAAGAAGGG	TTCTGTAACC	TCTA	844

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
45	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	250
	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300
	GCTCCAACCT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
50	GATCAAGGTT	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	500
	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
55	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
	CCATCAGCCG	TTGGTTACCA	ACCAAACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG			830

60

2) INFORMATION FOR SEQ ID NO: 953

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
20	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACTT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCAACAAC	450
	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

40 2) INFORMATION FOR SEQ ID NO: 954

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAAC	TTGATGAG	GTCTACCT	TCTGAAAT	CC	350
	GATCAAGG	ATTGACCT	TTGCCCCT	CCTTAAAG	GGTAAAG	400
	GACTTTTC	TGGTGCCG	GTTGGTAA	CTGTCTTA	CCAAGAAT	450
	ATTCACA	AT	TTGCCCA	GCACGGTG	TTGCTGGT	500
5	TGGGGAAC	CGT	ACTCGTG	GGAATGAC	CT	550
	CAGGCGTT	AT	CGAGAAA	GCCATGGT	CT	600
	CCAGGAGC	AC	GTATGCGT	TGCCCTTA	GGTTTGAC	650
	CTTCCGTG	AT	GTGGAAGG	AAGACGTG	TCTCTTTA	700
	TCCGTTTC	AC	TCAGGCTG	TCAGAAGT	AT	750
10	CCATCAGC	CG	TTGGTTAC	ACCAACAC	CT	800
	GCAAGAAC	CG	ATCACATC	CAAAGAAG	GG	844

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCTT	300
	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCAAGA	GCACGGTG	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTA	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CAAAGAAGGG	TTCTGTAACC	TCTA		834

50

2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microti*
 (B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGG TTCACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTAA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTTACTTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTCAGGAC	GTCTTGCGAG	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGCAGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

50 2) INFORMATION FOR SEQ ID NO: 958

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

```

5  TACAACACCA ACTTGCTAAA TGGGCAGATG CAGAAGTAGT TGTTTATGTT      50
   GGTGTGGGG AACGTGGAAA TGAAATGACC GATGTACTTA TGGAATTCCC      100
   AGAAATTATT GACCCTAAGA CAGGACAATC TTAAATGAAG AGAACAGTTC      150
   TTATAGCTAA TACTTCTAAT ATGCCAGTTG CTGCTCGTGA GGCTTCAATC      200
   TATACTGGTA TAACTATTGC AGAATATTTT AGAGATATGG GATATTCAGT      250
10 GGCACCTATG GCAGATTCAA CAAGTCGTTG GGCAGAAAGCA CTTCGTGAAA      300
   TGTCAGGACG TTTGGAAGAA ATGCCAGGTG ATGAAGGATA TCCAGCATAT      350
   CTATCAAGTA GAATAGCAGA GTTTTATGAA AGAGCAGGGC TTGTTGAATG      400
   TCTAGGTAAT GGAGAAGAAG GAGCATTAAC TGTAATTGGA GCAGTATCTC      450
   CA                                     452
15

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2) INFORMATION FOR SEQ ID NO: 959

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania aethiopica
30  (B) STRAIN: ATCC 50119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

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35  TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT      50
   ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100
   TTCCCGACCC TGACGACCGT GATCAATGGT CGCGAGGAGT CGATCATGAA      150
   GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
   AGGCCTCTAT TTACACCGGC ATCACCCTGG CCGAGTACTA CCGTGATATG      250
   GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
40  GCTTCGTGAG ATTTCTGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
   ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC      400
   CTCGTCACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
   CGGTGCCGTG TCTCCGCCG                                     469
45

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2) INFORMATION FOR SEQ ID NO: 960

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50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
55  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania tropica
60  (B) STRAIN: ATCC 30815

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
5	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
10	ACCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

15

2) INFORMATION FOR SEQ ID NO: 961

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania guyanensis</i>
(B)	STRAIN: ATCC 50126

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

	TGTCATCAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCGGAC	TGTGTCATCT	50
	ATGTCGGCTG	CGGTGAACGC	GGTAACGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACTGT	GATCGATGGT	CGCGAAGAGT	CCATCATGAA	150
35	GCGCACCTGC	CTCGTGCGGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTATACCGGC	ATCACCTTGG	CTGAGTACTA	CCGTGATATG	250
	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTGCGTGAG	ATTTCGGGTC	GATTGGCGGA	GATGCCGGCT	GATGGTGGCT	350
	ACCTGCCTA	CCTCAGCGCC	CGCCTCGCCT	CCTTCTACGA	GCGCGCCGGT	400
40	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCAGTG	TCTCCACCG				469

45 2) INFORMATION FOR SEQ ID NO: 962

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
	(B) TYPE: Nucleic acid
50	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania donovani</i>
(B)	STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

60

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCCACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCAGTC	GCAGCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TTCCCGACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCCAA	CATGCCAGTT	GCAGCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCCACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCCGGTTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
40	TGGTGCGGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 964

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania mexicana*
 55 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

	TTCCCGACCC	TGACGACCAT	GATCGATGGT	CGGGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACCTCGAA	CATGCCCCGTC	GCAGCCCCGTG	200
	AGGCCTCTAT	CTACACCGGC	ATCACCCCTCG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCTGAGGC	300
5	GCTTCGTGAG	ATTTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCCGTG	TCTCCGCCG				469

10

2) INFORMATION FOR SEQ ID NO: 965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
30	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
35	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

40

2) INFORMATION FOR SEQ ID NO: 966

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 449 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

	CACCAGTTCG	CCAAGTGGGC	AGATGCTCAG	ATAGTTGTAT	ACGTTGGTTG	50
	TGGAGAACGT	GGTAACGAGA	TGACAGACGT	TCTAAATGAA	TTCCCAAGAA	100
	TGATTGACCC	TCATACAGGC	GAATCTCTAA	TGAAGAGAAC	AGTTCTTATA	150
60	GCTAATACGT	CAAATATGCC	AGTTGCAGCC	AGAGAGGCAA	GTATATATAC	200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCAAC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: ATCC 9797

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCTG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTC	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCTG	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCTGA	CGGTGCGTTC	CTGATGCCGG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCCGTG	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGTACATT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: BD180

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

	CGATCCTGGT	GGTGTCTGGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTTCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCG	CGAACTGCTG	AGCAAGTACG	ATTTCCCGGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTG	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGGTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCACG	GTGGTGACTG	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAGAC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATCGCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTAAGTTGAA	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTCT	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTGAAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCCTGCT	TGAAGTGTAC	600
50	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

2) INFORMATION FOR SEQ ID NO: 970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
10	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAACGT	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTTGG	50
	TGTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAA	AAGCAGTTGT	TACTGGTGTT	450
50	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

```

15 TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA GCACATCCTG      50
   CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC TGAACAAATG      100
   CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA ATGGAAGTTC      150
   GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC TCCGATCGTT      200
20 CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT GGAAGCGAA      250
   AATCCTGGAA CTGGCTGGCT TCCTGGATTG TTACATTCCG GAACCAGAGC      300
   GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT ATTCTCCATC      350
   TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG GTATCATCAA      400
   AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT CAGAAGTCTA      450
25 CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA AGGCCGTGCT      500
   GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG AAGAAATCGA      550
   ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG CACACCAAGT      600
   TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG CCGTCATACT      650
   CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA CTACTGACGT      700
30 GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA ATGCCGGGCG      750
   ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC GATGGACGAC      800
   GGT                                     803

```

2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

```

   ACTGACGGCC CGATGCCGCA GACTCGTGAG CACATCCTGC TGGGTCGTCA      50
   GGTAGGCGTT CCGTACATCA TCGTGTTTCT GAACAAATGC GACATGGTTG      100
   ATGACGAAGA GCTGCTGGAA CTGGTTGAAA TGGAAGTTTC TGAAGTTCTG      150
55 TCTCAGTACG ACTTCCCGGG CGACGACACT CCGATCGTTC GTGGTTCTGC      200
   TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG GGAAGCGAAA ATCCTGGAAC      250
   TGGCTGGCTT CCTGGATTCC TACATTCCGG AACCAGAGCG TGCRAATTGAC      300
   AAGCCGTTCC TGCTGCCGAT CGAAGACGTA TTCTCCATCT CCGGTCGTGG      350
   TACCGTTGTT ACCGGTCGTG TAGAACGCGG TATCATCAAA GTTGGTGAAG      400
60 AAGTTGAAAT CGTTGGTATC AAAGAGACTC AGAAGTCTAC CTGTACTGGC      450

```

GTGAAATGT	TCCGCAAAC	GCTGGACGAA	GGCCGTGCTG	GTGAGAACGT	500
AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	AGAAATCGAA	CGTGGTCAGG	550
TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	ACACCAAGTT	CGAATCTGAA	600
GTGTACATTC	TGTCCAAAGA	TGAAGGCGGC	CGTCATACTC	CGTTCTTCAA	650
5 AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	TACTGACGTG	ACTGGTACCA	700
TTGAACTGCC	GGAAGGCGTA	GAGATGGTAA	TGCCGGGCGA	CAACATCAAA	750
ATGGTTGTTA	CC				762

10

2) INFORMATION FOR SEQ ID NO: 974

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 11775

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

CCTGGTAGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACT	CGTGAGCACA	50
TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGCTG	TTGAAATGGA	150
30 AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCCTACA	TTCCGGAACC	300
AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
35 ATCAAAGTTG	TGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GCGGTATCAA	ACGTGAAGAA	550
ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGTCGTC	650
40 ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
ACGA					804

45

2) INFORMATION FOR SEQ ID NO: 975

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

```

5   GCGATCCTGG TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA      50
    GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC      100
    TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA      150
    ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC      200
    TCCGATCGTT CGTGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT      250
    GGGGAAGCGAA AATCCTGGAA CTGGCTGGCT TCCTGGATTC YTACATTCCG      300
    GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT      350
10  ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG      400
    GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT      450
    CAGAAGTCTA CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
    AGGCCGTGCT GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG      550
    AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG      600
15  CACACCAAGT TCGAATCTGA AGTGATACATT CTGTCCAAAG ATGAAGGCGG      650
    TCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA      700
    CTACTGACGT GACTGGTACC ATCGAACTGC CGGAAGGTGT AGAGATGGTA      750
    ATGCCGGGCG ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC      800
    GATG                                                                804
20

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2) INFORMATION FOR SEQ ID NO: 976

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25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Mycobacterium avium
35  (B) STRAIN: Mavi-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

```

40  GGCGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTCGG TGTGCCCTAC ATCCTGGTCG      100
    CCCTGAACAA GGCCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC      150
    GAGATGGAGG TCCGCGAGCT GCTGGCCGCC CAGGAGTTCG ACGAGGACGC      200
    CCCGGTGGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGC GACGCCAAGT      250
    GGGTCGAGTC CGTCGAGCAG CTGATGGAGG CCGTCGACGA GTCGATCCCG      300
45  GACCCGGTCC GCGAGACGGA GAAGCCGTTT CTGATGCCGG TGGAGGACGT      350
    CTTACCATC ACCGGGCGTG GCACCGTGGT CACCGGTCGT GTCGAGCGCG      400
    GTGTGATCAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CCGCCCGACC      450
    AGCACCAAGA CCACGGTCAC CGGTGTGGAR ATGTTCCGCA AGCTGCTCGA      500
    CCAGGGCCAG GCCGGTGACA ACGTCGGTCT GCTGCTGCGT GGTATCAAGC      550
50  GTGAGGACGT CGAGCGCGGC CAGGTCGTGA CCAAGCCCGG CACCACCACG      600
    CCGCACACCG AGTTCGAGGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
    CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC      700
    GCACCACCGA CGTGACCGGT GTGGTGACGC TGCCGGAGGG CACCGAGATG      750
    GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGCTGA TCCAGCCCGT      800
55  CGCCATGGAC GACGGTSTGC GGTTC                                                                825

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2) INFORMATION FOR SEQ ID NO: 977

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

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15 TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
   ACATCCTTCT TTCACGTCAG GTTGGTGTGA AACACCTTAT CGTCTTCATG      100
   AACAAAGTTG ACTTGGTGTA CGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
   GGAAATCCGT GACCTATTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
   CAGTTATCCA AGGTTCAGCA CTTAAAGCTC TTGAAGGTGA CTCTAAATAC      250
20 GAAGACATCG TTATGGAATT GATGAACACA GTTGATGAGT ATATCCCAGA      300
   ACCAGAACGT GACACTGACA AACCATTGCT TCTTCCAGTC GAGGACGTAT      350
   TCTCAATCAC TGGACGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
   ATCGTTAAAG TCAACGACGA AATCGAAATT GTTGGTATCA AAGAAGAAAC      450
   TCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAACTTGACG      500
25 AAGGTCTTGC TGGAGATAAC GTAGGTGTCC TTCTTCGTGG TGTTCACGT      550
   GATGAAATCG AACGTGGACA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
   ACACACTAAA TTCAAAGGTG AAGTCTACAT CCTTACTAAA GAAGAAGGTG      650
   GACGTCACAC TCCATTCTTC AACAACCTACC GTCCACAATT CTACTTCCGT      700
   ACTACTGACG TTACAGGTTC AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
30 AATGCCTGGT GATAACGTGA CAATCGACGT TGAGTTGATT CACCCAATCG      800
   CCGTAGAACA AGGTACTACA                                820

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35 2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

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50 GGCGCGATCC TGGTGGTCGC CGCCACCGAT GGCCCGATGC CGCAGACCCG      50
   TGAGCACGTG CTGCTCGCCC GTCAGGTGGG CGTGCCCTAC ATCCTGGTGG      100
   CGCTGAACAA GTCCGACGCG GTCGACGACG AGGAGCTGCT CGAGCTCGTC      150
   GAGCTGGAGG TCCGCGAGTT GCTGGCCGCC CAGGACTTCG ACGAGGAAGC      200
55 TCCGGTGGTC CGGGTCTCGG CGCTGAAGGC GCTCGAGGGC GACGCCACCT      250
   GGGTGAAGTC GGTAGAGGAC TTGATGGACG CGGTGACGCA GTCGATTCCG      300
   GACCCGGTCC GCGACACCGA CAAGCCGTTC CTGATGCCCG TCGAGGACGT      350
   CTTACCATC ACCGGTCGTG GCACCGTCGT CACCGGCCGT GTGGAGCGCG      400
   GCGTGGTGAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CAAGCCGACC      450
60 AGCACCAAGA CCACGGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500

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	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCGG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCCG	800
	CGCCATGGAC	GACGGTCTGC	GG			822

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2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-11

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTG GTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGG TTCAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACTTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAAC TAC	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	A			821

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2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: ATCC 25177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

	GGTGC	GATCC	TGGTGG	TGCG	CGCCAC	CGAC	GGCCCC	GATGC	CCCAG	ACCCG	50
	CGAGC	ACGTT	CTGCT	GGCG	GTCAAG	TGGG	TGTGCC	CTAC	ATCCT	TGGTAG	100
5	CGCTG	AACAA	GGCCG	ACGCA	GTGGAC	GACG	AGGAG	CTGCT	CGAACT	CGTC	150
	GAGAT	GGAGG	TCCGC	GAGCT	GCTGG	CTGCC	CAGGA	ATTCT	ACGAG	GACGC	200
	CCCGG	TTGTG	CGGGT	CTCG	CGCTCA	AGGC	GCTCG	AGGGT	GACGC	GAAGT	250
	GGGTT	GCCTC	TGTCG	AGGAA	CTGAT	GAAAC	CGGTC	GACGA	GTCGAT	TCCG	300
	GACCC	GGTCC	GCGAG	ACCGA	CAAGCC	GTTC	CTGAT	GCCGG	TCGAG	GACGT	350
10	CTTCAC	CATT	ACCGG	CCGC	GAACCG	TGGT	CACCG	GACGT	GTGGAG	CGCG	400
	GCGTG	ATCAA	CGTGA	ACGAG	GAAGTT	GAGA	TCGTC	GGCAT	TCGCC	CATCG	450
	ACCAC	CAAGA	CCACCG	TCAC	CGGTGT	GAG	ATGTT	CCGCA	AGCTG	CTCGA	500
	CCAGG	GCCAG	GCGGG	GACA	ACGTT	GTTT	GCTG	CTGCG	GGCGT	CAAGC	550
	GCGAG	GACGT	CGAGC	GTGGC	CAGGT	TGTCA	CCAAG	CCCCG	CACCAC	CACG	600
15	CCGCAC	ACCG	AGTTC	GAAG	CCAGGT	CTAC	ATCCT	GTCCA	AGGAC	GAGGG	650
	CGGCC	GGCAC	ACGCC	GTTCT	TCAACA	ACTA	CCGT	CCGCA	TTCTAC	TTC	700
	GCACC	ACCGA	CGTGAC	CGGT	GTGGT	GACAC	TGCCG	GAGGG	CACCG	GAGATG	750
	GTGAT	GCCCC	GTGACA	ACAC	CAACAT	CTCG	GTGA	AGTTGA	TCCAG	CCCCG	800
20	CGCCAT	GAC	GAAGG	TNTGC	GTTTC	GCG					828

2) INFORMATION FOR SEQ ID NO: 981

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 819 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
30	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Staphylococcus warneri</i>
35	(B) STRAIN: CSG 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

	CGGCG	GTATC	TTAGTA	GTAT	CTGCT	GCAGA	TGGCCC	AATG	CCACAA	AACTC	50
40	GTGAAC	ACAT	CTTATT	ATCA	CGTAAC	GTTG	GTGTAC	CAGC	TTTAGT	TGTA	100
	TTCTT	AAACA	AAGCT	GACAT	GGTTG	ACGAC	GAAGA	ATTAT	TAGAAT	TAGT	150
	TGAAAT	TGGAA	GTTCT	GACT	TATTAT	CTGA	ATACG	ACTTC	CCTGGT	GACG	200
	ATGTAC	CAGT	TATCG	TTGGT	TCTGC	ATTAA	AAGCT	TTAGA	AGGCG	ACCCA	250
	GAATAC	GAAAC	AAAAA	ATCTT	AGACT	TAAATG	CAAGC	TGTAG	ATGACT	TACAT	300
45	CCCAACT	CCA	GAACG	TGACT	CTGATA	AAACC	ATTCAT	GATG	CCAGTT	GAGG	350
	ACGTATT	CTC	AATCA	CTGGT	CGTGG	TACTG	TAGCA	ACAGG	CCGTGT	TGAA	400
	CGTGGT	CAAA	TCAAAG	TGCG	TGAAGA	AGTT	GAAAT	CATCG	GTATCA	CTGA	450
	AGAAAG	CAAG	AAAACA	ACAG	TTACAG	GTTG	AGAAAT	GTTC	CGTAA	ATTAT	500
	TAGACT	TACG	TGAAG	CTGGT	GACAAC	ATCG	GTGCT	TTATT	ACGTGG	TGTT	550
50	GCACGT	GAAAG	ACGTACA	ACG	TGGACA	AGTA	TTAGC	AGCTC	CTGGCT	CTAT	600
	TACTCC	CACAC	ACAAA	ATTCA	AAGCT	GATGT	TTACG	TTTTA	TCTAA	AGAAG	650
	AAGGT	TGGACG	TCATA	CTCCA	TTCTT	CACTA	ACTAC	GCCC	ACAATT	CTAC	700
	TTCCG	TACTA	CTGAC	GTAAC	TGGCG	TTGTT	CACTT	ACCAG	AAGGT	ACTGA	750
	AATGG	TTATG	CCTGG	CGATA	ACGTAG	AAAT	GACTG	TTGAA	TTAAT	CGCTC	800
55	CAATC	GCGAT	TGAAG	ACGG							819

2) INFORMATION FOR SEQ ID NO: 982

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

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15  CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
    CACATCCTTC TTTCACGTCA GGTGTTGTTT AAACACCTTA TCGTCTTCAT      100
    GAACAAGATC GACTTGTTTG ATGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
    TGGAAATCCG TGACCTCTTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
    CCAGTTATCC AAGGTTTCAGC TCTTAAAGCT CTTGAAGGTG ATACTAAGTA      250
20  CGAAGACATC ATCATGGAAT TGATGAACAC TGTTGATGAG TACATCCCAG      300
    AACCAGAACG TGACTCTGAC AAACCTCTTC TTCTTCCAGT CGAAGACGTA      350
    TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
    TACTGTTTCG GTCAACGATG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
    TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAGCTTGAC      500
25  GAAGGTCTTG CAGGGGACAA CGTAGGTGTA CTTCTTCGTG GTATCCAACG      550
    TGATGAAATC GAACGTGGTC AAGTTATCGC TAAACCAGGT TCAATCAACC      600
    CACACACTAA ATTCAAGGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT      650
    GGACGTCACA CTCCATTCTT CAACAACACT CGTCCACAGT TCTACTTCCG      700
    TACAACTGAC GTTACAGGTT CAATCGAACT TCCAGCAGGT ACTGAAATGG      750
30  TAATGCCTGG TGATAACGTA ACTATCGACG TTGAGTTGAT CCACCCAATC      800
    GCCGTTGAAC AAGG                                     814
  
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35 2) INFORMATION FOR SEQ ID NO: 983

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

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50  CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
    CACATCCTTC TTTCACGTCA GGTGTTGTTT AAACACCTTA TCGTCTTCAT      100
    GAACAAAGTT GACTTGTTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
    TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
55  CCAGTTATCC AAGGTTTCAGC TCTTAAAGCC CTTGAAGGTG AACTAAATA      250
    CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG      300
    AACCAGAACG TGACACTGAC AAACCATTCG TTCTTCCAGT CGAAGACGTA      350
    TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
    TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
60  CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC      500
  
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	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC					810

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2) INFORMATION FOR SEQ ID NO: 984

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTAGT	AGCTTCAACT	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCCTTCTTT	CACGTCAGGT	TGGTGTTAAA	CACCTTATCG	TCTTCATGAA	100
	CAAGATCGAC	TTGGTTGATG	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	150
30	AAATCCGTGA	CCTCTTGTC	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	200
	GTTATCCAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGTGATA	CTAAGTACGA	250
	AGACATCATC	ATGGAATTGA	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	300
	CAGAACGTGA	TACTGACAAA	CCTCTTCTTC	TTCCAGTCGA	AGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	400
35	TGTTTCGTGTC	AACGATGAAA	TCGAAATCGT	TGGTATCAAA	GAAGAAATCC	450
	AAAAAGCAGT	TGTTACTGGT	GTTGAAATGT	TCCGTAAACA	GCTTGACGAA	500
	GGTCTTGCAG	GGGACAACGT	AGGTGTAATT	CTTCGTGGTA	TCCAACGTGA	550
	TGAAATCGAA	CGTGGTCAAG	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	600
	ACACTAAATT	CAAGGGTGAA	GTTTACATCC	TTACTAAAGA	AGAAGGTGGA	650
40	CGTCACACTC	CATTCTTCAA	CAACTACCGT	CCACAGTTCT	ACTTCCGTAC	700
	AACTGACGTT	ACAGGTTCAA	TGAACTTCC	AGCAGGTACT	GAAATGGTAA	750
	TGCCTGGTGA	TAACGTAAC	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	800
	GTTGAACAAG	GTACTAC				817

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2) INFORMATION FOR SEQ ID NO: 985

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTTAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTC	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	G TTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCGA	AGACGTATTC	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTCTGTGC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACTTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

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2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
	CTTCTTTCAC	GTCAGGTG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

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2) INFORMATION FOR SEQ ID NO: 987

(i) SEQUENCE CHARACTERISTICS:

549

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

15	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAA	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCGATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTCTGGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTC	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTAATATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCCTGTTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAAGT	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTACTGAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45 2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

	GGATCCTGTA	TATGCACAAA	AACTAGGTGT	TAACATCGAT	GAATTACTAT	50
	TATCACAACC	TGATACAGGG	GAGCAAGGT	TAGAAATCGC	AGAAGCACTT	100
	GTACGAAGTG	GTGCGGTTGA	TATTATCGTA	ATTGACTCTG	TAGCAGCTCT	150
5	TGTA					154

2) INFORMATION FOR SEQ ID NO: 991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella melaninogenica*
- (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25	GCCATTGCAG	AGGCACAGAA	GCAGGGCGGT	ATTGCAGCCT	TCATTGATGC	50
	TGAGCACGCC	TTCGACCGTT	TCTATGCAGA	GAAGTTAGGT	GTGGATGTTG	100
	ATAACCTTTG	GGTTTCACAG	CCAGACAATG	GTGAGCAGGC	TTTAGAGATT	150
	GCCGACCAGC	TGATTTCGCTC	TTCCGCTATT	GACATTCTCG	TTGTCGACTC	200
	AGTTGCAGCC	TTGACTCCAA	AGAAGGAGAT	TGAGGGTGAC	ATGGGTGACT	250
30	CTGCAGTAGG	TTTACAAGCA	CGACTGATGA	GTCAGGCATT	GCGTAAACTT	300
	ACCTCAACAA	TCGCAAAAAC	TAATACTTGC	TGCATCTTCA	TCAACCAGTT	350
	GCGTGAGAAG	ATTGGTGTGA	TGTTTGGTAA	TCCA		384

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	CATACATCGT	50
	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	TTACTAGAAT	100
	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	CTTCCCAGGC	150
55	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	TTGAAGGCGA	200
	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	GTTGACGAAT	250
	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	GATGCCAGTC	300
	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	CAGGCCGTGT	350
	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	GTTGGTATTG	400
60	CTGAAGAAAC	TGCTAAAACA	ACTGTAAC TG	GTGTTGAAAT	GTTCCGTAAA	450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: extracted from U40453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTTAGT	50
25 GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAAC TTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCTGTT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAAC TTAAGA	ACCAAGAGAT	GGCAACTTTA	300
30 TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTTAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
35 CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACCAACC	750
40 AAGTAA					756

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995

ACATTCTCGT GAGTAACAGG GT

2) INFORMATION FOR SEQ ID NO: 996

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996

ACAAATCATG AAGGGAATCA TTTAG

2) INFORMATION FOR SEQ ID NO: 997

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997

CTAATTCTTG AGCAGTTACC ATT

2) INFORMATION FOR SEQ ID NO: 998

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998

GGAGGGGTAA CAAATCATGA AGG

2) INFORMATION FOR SEQ ID NO: 999

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999

15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000

30 TTAGTGTGTG GGTTGATTGA ACT

23

2) INFORMATION FOR SEQ ID NO: 1001

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001

AAGAGTTGCT TGAATTAGTT GAG

23

2) INFORMATION FOR SEQ ID NO: 1002

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

	AACATGATCA	CTGGTGCCGC	TCAAATGGAC	GGAGCTATCC	TTGTAGTTGC	50
	TTCAACTGAT	GGACCAATGC	CACAACTCG	TGAGCACATC	CTTCTTTCAC	100
	GTCAGGTTGG	TGTTAAACAC	CTTATCGTGT	TCATGAACAA	AGTTGACCTT	150
10	GTTGATGACG	AAGAGTTGCT	TGAATTAGTT	GAGATGGAAA	TTCGTGACCT	200
	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	CCTTCCAGTT	ATCCAAGGTT	250
	CAGCTCTTAA	AGCTCTTGAA	GGCGACACTA	AATTTGAAGA	CATCATCATG	300
	GAATTGATGG	ATACTGTTGA	TTCATACATT	CCAGAACCAG	AACGCGACAC	350
	TGACAAACCA	TTGCTTCTTC	CAGTCGAAGA	CGTATTCTCA	ATTACAGGTC	400
15	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTACTGT	TCGTGTCAAC	450
	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	AAGCTGTTGT	500
	TACTGGTGT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCAGGAG	550
	ACAACGTAGG	TATCCTTCTT	CGTGGTGTTC	AACGTGACGA	AATCGAACGT	600
	GGTCAAGTTA	TTGCTAAACC	AAGTTCAATC	AACCCACACA	CTAAATTCAA	650
20	AGGTGAAGTA	TATATCCTTT	CTAAAGACGA	AGGTGGACGT	CACACTCCAT	700
	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACAAC	TGACGTAACA	750
	GGTTCAATCG	AACTTCCAGC	AGGTACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CGTGACAATC	AACGTTGAGT	TGATCCACCC	AATCGCCGTA	GAACAAGGTA	850
25	CTACTTTCTC	AATCCGTGAA	GGTGGACGTA	CTGTTGGTTC	AGGT	894

2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

	AATGGATCCT	GTATATGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTAC	50
45	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTAGAAAT	CGCGGAAGCA	100
	CTTGTACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGTACCG	AAAGCAGAGA	TTGAAGGCGA	CATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTCTGAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CAAAAACAAT	TGCAATCTTT	ATTAACCAA	TTCGTGAAAA	300
50	AGTTGGGGTT	ATGTTCTCGAA	ACCCAGAAAC	AA		332

2) INFORMATION FOR SEQ ID NO: 1004

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

10	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
15	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
20	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
25	CTCAAGCTGG	TAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
30	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CC				1212

35

2) INFORMATION FOR SEQ ID NO: 1005

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
55	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
60	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTCGGTAA	TATTACTCTG	350

	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTTGC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTGC	TTACATGATG	ACCGAAATGA	TGAAAACTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1213 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-03
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
55	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
 CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1218 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
25	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
30	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
35	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
40	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
45	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCTGATC				1218

50 2) INFORMATION FOR SEQ ID NO: 1008

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1223 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

5	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	150
	AGTAACGTTT	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	200
10	GGGTTCTGCT	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	250
	GTGTTTATGA	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	300
	CCGGGAACAA	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTTCGGTAA	350
	TATTACTCTG	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
15	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	TACAACAGAA	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCTTATGC	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	600
	ATCCATAAAG	TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	650
	CGGAACCTCG	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	700
20	TGAAAACAGT	CTTGACTTAT	GGAACCTGGC	GTGGAGCCTA	TCTTCCTTGG	750
	CTTCCTCAAG	CTGGTAAAAC	AGGAACCTCT	AACATACAG	ATGAGGAAGT	800
	TGAAAACCAAC	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	850
	TTGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
25	TCGCTCAATG	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	1000
	CGATGCCAGA	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	1050
	GCTCGCCCAA	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
30	CAATCAAATA	CAACCCCTGA	TCA			1223

2) INFORMATION FOR SEQ ID NO: 1009

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1214 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
40	(D) TOPOLOGY: Linear
	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
45	(A) ORGANISM: <i>Streptococcus pneumoniae</i>
	(B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

50	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
55	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACCTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
60	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550

	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
15	CAAATACAAC	CCCT				1214

2) INFORMATION FOR SEQ ID NO: 1010

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1223 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACTTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTCA	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

2) INFORMATION FOR SEQ ID NO: 1011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
TGCCTTTTGA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
CTTGACTTAT	GGAACCTGGC	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
CTGGTAAAAC	AGGAACCTCT	AACTATACAG	ATGAGGAAGT	TGAAAACCAC	800
ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCC					1207

2) INFORMATION FOR SEQ ID NO: 1012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATAAC	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
20	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AAATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGAACCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTGTC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTTCGGTA	CCAACCAGGC	CGTAGAAACC	AATCGTGACT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGACT	ATGCTCCCGC	TTAGAAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACAACCTG	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	500
	ACACAACCTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GACTGAAATG	700
60	ATGAAAACCTG	TTTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAAGTATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATAACAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

15

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1199 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCCTTGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAACT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

55

2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 1211 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-12

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCCGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATAACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

40

2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-13

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAA	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACCTGT	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1229 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCGAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGG	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTGCTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACCTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTCTGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAACT	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCAC	ACTCAAATGC	TATTTCAAGT	500
35	AATACAACTG	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCT	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTACTT	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAGT	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAA	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
	AACAATCAAA	TACAACCCCT	GATCA			1225

50

2) INFORMATION FOR SEQ ID NO: 1019

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

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10 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTGGAACC TCCTATTTGG AAAAGCAATA      200
   TGAAGAGACC TTACAAGGAA AACGCTCGGT AAAAGAAATC CATCTGGATA      250
   AATATGGCAA TATGGAAAGC GTGGACACAA TTGAGGAAGG TAGTAAGGGA      300
15  AACAATATCA AACTGACCAT TGATTTGGCC TTCCAAGATA GCGTGGATGC      350
   TTTGCTGAAA AGTTATTTCA ATTCCGAGCT AGGAAATGGT GGAGCTAAAT      400
   ATTCTGAAGG TGTCTATGCA GTCGCCCTTA ACCCAAAAAC AGGTGCTGTT      450
   TTATCCATGT CAGGGATCAA ACATGACCTG AAAACGGGAG AGTTGACTCC      500
   TGATTCCTTG GGAACGGTAA CCAATGTCTT TGTCCCAGGT TCGGTTGTCA      550
20  AGGCTGCGAC CATCAGCTCA GGTGGAAGAA ATGGTGTTTT ATCAGGAAAC      600
   CAAACCTTAA CAGATCAGCC TATTGTTTTT CAAGGTTTCA CTCCAATTTA      650
   TTCTTGGTAT AAATTGGCAT ATGGATCTTT TCCTATTACA GCTGTGGAAG      700
   CCTTGAGTA TTCATCCAAT GCTTACATGG TTCAAACCGC TCTTGAATC      750
   ATGGGCCAGA CCTATCAACC AAATATGTTT GTTGAACCA GCAATTGGA      800
25  AACAGCTATG GGAAACTTC GTGCGACCTT TGGCGAATAT GGCTTGGGGG      850
   CTGCGACCGG AATTGACCTA CCAGATGAAT CTACTGGATT TGTTCCCAA      900
   GAGTATAGCT TTGCTAATTA CATACCAAT TCCTTTGGGC AGTTTGATA      950
   CTATACGCC ATGCAGTTGG CTCAGTATGT AGCAACTATT GCAAATAATG      1000
   GTGTTCTGT GGCTCCTCGT ATTGTTGAAG GCATTTATGG TAATAATGAT      1050
30  AAGGGAGGAC TGGGTGACTT GATTGAGCAA CTGCAACCGA CAGAGATGAA      1100
   TAAGGTCAAT ATATCCGACT CCGATATGAG CATCTTGCAC CAAGGTTTTT      1150
   ATCAGGTTGC CCATGGTACT AGTGGATTGA CAACTGGACG TGCCTTTTCA      1200
   AATGGTGCCT TGGTATCCAT TAGCGGAAAA ACAGGTACAG CCGAAAGCTA      1250
   TGTGGCAGAT GGTCAGCAAG CAACCAATAC CAATGCGGTG GCCTATGCCC      1300
35  CATCTGATAA TCCCCAAATC GCTGTCGCAG TGGTCTTTCC TCATAATACC      1350
   AATCTAACAA ATGGTGTAGG ACCTTCCATT GCGCGTGACA TTATCAATCT      1400
   GTATCAAAAA TACCATCCAA TGAAC TAGAA      1439

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40 2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

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60 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTGGAACC TCCTATTTGG AAAAGCAATA      200

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	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCAG	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACCTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTTCAGCA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCC	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTCGCAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAACTAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

15

2) INFORMATION FOR SEQ ID NO: 1022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTCC	AAGGTTTCAGC	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGGAGTAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACCAAG	CAATTTGGAA	ACAGCTATGG	800
	GAAAACTTCG	TGCACCTTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCTGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGCACC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTGCGAGT	GGTCTTTCCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

570

2) INFORMATION FOR SEQ ID NO: 1023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT	TCAAAGGAGA	TGCCTGGCAT	TAGTATTTCT	ACTTCTTGGG	50
	ATCGAAAGGT	TTTGAAACT	TCCCTTTCTT	CTATAGTAGG	GAGTGTATCC	100
	AGTGAAAAAG	CTGGTCTCCC	AGCGGAAGAA	GCAGAATCCT	ATCTTAAAAA	150
	AGGCTATTCT	CTAAATGACC	GTGTTGGAAC	CTCCTATTTG	GAAAAGCAAT	200
	ATGAAGAGAC	CTTACAAGGA	AAACGCTCGG	TAAAAGAAAT	CCATCTGGAT	250
25	AAATATGGCA	ATATGGAAAG	CGTGGACACA	ATTGAGGAAG	GTAAGGGA	300
	AAACAATATC	AAACTGACCA	TTGATTGTC	CTTCCAAGAT	AGCGTGGATG	350
	CTTTGCTGAA	AAGTTATTTT	AATTCCGAGC	TAGGAAATGG	TGGAGCTAAA	400
	TATTCTGAAG	GTGTCTATGC	AGTCGCCCTT	AACCCAAAAA	CAGGTGCTGT	450
	TTTATCCATG	TCAGGGATCA	AACATGACCT	GAAAACGGGA	GAGTTGACTC	500
30	CTGATTCCTT	GGGAACGGTA	ACCAATGTCT	TTGTCCCAGG	TTCGGTTGTC	550
	AAGGCTGCGA	CCATCAGCTC	AGGTTGGGAA	AATGGTGTTC	TATCAGGAAA	600
	CCAAACCTTA	ACAGATCAGC	CTATTGTTTT	CCAAGTTTCA	GCTCCAATTT	650
	ATTCTTGATA	TAAATTGGCA	TATGGATCTT	TTCCTATTAC	AGCTGTGGAA	700
	GCCTTGAGAT	ATTCATCCAA	TGCTTACATG	GTTCAAACCG	CTCTTGGAAT	750
35	CATGGGCCAG	ACCTATCAAC	CAAATATGTT	TGTTGGAACC	AGCAATTTGG	800
	AAACAGCTAT	GGGAAAACCT	CGTGCGACCT	TTGGCGAATA	TGGCTTGGGG	850
	GCTGCGACCG	GAATTGACCT	ACCAGATGAA	TCTACTGGAT	TTGTTCCCAA	900
	AGAGTATAGC	TTTGCTAATT	ACATCACCAA	TTCCTTTGGG	CAGTTTGATA	950
	ACTATACGCC	CATGCAGTTG	GCTCAGTATG	TAGCAACTAT	TGCAAATAAT	1000
40	GGTGTTCGTG	TGGCTCCTCG	TATTGTTGAA	GGCATTATAT	GTAATAATGA	1050
	TAAGGGAGGA	CTGGGTGACT	TGATTCAGCA	ACTGCAACCG	ACAGAGATGA	1100
	ATAAGGTCAA	TATATCCGAC	TCCGATATGA	GCATCTTGCA	CCAAGGTTTT	1150
	TATCAGGTTG	CCCATGGTAC	TAGTGGATTG	ACAACCTGGAC	GTGCCTTTTC	1200
	AAATGGTGCC	TTGGTATCCA	TTAGCGGAAA	AACAGGTACA	GCCGAAAGCT	1250
45	ATGTGGCAGA	TGGTCAGCAA	GCAACCAATA	CCAATGCGGT	GGCCTATGCC	1300
	CCATCTGATA	ATCCCCAAAT	CGCTGTCGCA	GTGGTCTTTC	CTCATAATAC	1350
	CAATCTAACA	AATGGTGTAG	GACCTTCCAT	TGCGCGTGAC	ATTATCAATC	1400
	TGTATCAAAA	ATACCATCCA	ATGAAGTAGA	AAGGAAATTA	TG	1442

2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTTGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAAC TGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTC CGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTTATCCAT	GTCAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTCC CAG	GTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGTGTT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGAGG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC T	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTC CCA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACCA	ATTCCTTTGG	GCAGTTTGAT	950
	AACTATACAC	CCATGCAGTT	GGCTCAGTAT	G TAGCAACTA	TTGCAAATAA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATT CAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AAATCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAAGTAG	AAAGGAAATT	ATGCT	1445

40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

55	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGA	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTTGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAAC TGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTT	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAACT	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AACTATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTTCAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	TGGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
25	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441

2) INFORMATION FOR SEQ ID NO: 1026

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAAC TGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCCGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGATAG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTTCGGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
50	CAAAGAGTAT	AGCTTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTAAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGC	1446

2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATAGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCTT	TGGGAACGGT	AACCAATGTC	TTTGTTCAG	GTTCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGACCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTT	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TTCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTGG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCG	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTTCAG	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACTGGC	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1447 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

55	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCGAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
25	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGCT	1447

2) INFORMATION FOR SEQ ID NO: 1031

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCTTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTGGA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GACTGGGTGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAACATA	GAAAGGAAAT	TATGCT	1446

15

2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAA	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGTATTT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACCTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

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5      GGAAACTGCA GAGGTCAAGG GGATTGATTT TACAACCAGT CCCAATCGTA      50
      GTTATCCAAA CGGACAATTT GCTTCTAGTT TTATCGGACT AGCTCAGCTC      100
10     CATGAAAATG AAGATGGCAG CAAGAGCTTA CTGGGAACCT CTGGAATGGA      150
      GAGTTCCTTG AACAGTATTC TTGCAGGGAC AGACGGTATT ATTACCTATG      200
      AAAAAGACCG TGTAGGAAAT ATCGTACCAG GTACAGAACT GGTATCGCAA      250
      CAAACTGTGG ATGGCAAGGA TGTTTATACA ACATTGTCTA GTCCGCTACA      300
      ATCTTTCATG GAAACTCAGA TGGATGCCTT TCTAGAAAAA GTAAAAGGTA      350
15     AGTATATGAC CGCGACCTTG GTCAGTGCAA AGACCGGTGA AATCCTCGCT      400
      ACCACCCAAC GACCTACCTT TAATGCAGAT ACTAAGAAG GAATCACTGA      450
      GGACTTTGTT TGGCGTGATA TTCTTTATCA AAGTAACTAT GAACCAGGAT      500
      CAGCCATGAA GGTTATGACG TTAGCTTCTT CTATTGATAA TAATACCTTC      550
      CCAAGTGGAG AATACTTCAA TAGCAGTGAA TTCAAAATAG CGGATGCGAC      600
20     GACTCGAGAT TGGGATGTTA ATGATGGTTT GACTACTGGT GGGATGATGA      650
      CTTTCTTACA AGGTTTCGCT CACTCCAGTA ATGTTGGAAT GAGTCTACTT      700
      GAACAAAAAA TGGGAGATGC TACTTGGTTG GATTATCTAA AACGCTTTAA      750
      ATTTGGGGTT CCAACTCGCT TTGGCTTGAC AGATGAATAC GCTGGTCAAC      800
      TTCCAGCTGA TAATATTGTT AGTATTGCTC AAAGCTCATT TGGGCAAGGA      850
25     ATTTCAGTGA CACAAACACA AATGCTTCGT GCCTTTACAG CTATTGCTAA      900
      TGATGGAGTT ATGCTGGAGC CAAAATTTAT AAGTGCTATT TATGATACTA      950
      ACAATCAGTC TGTACGTAAG TCACAAAAAG AAATAGTAGG AAATCCTGTT      1000
      TCCAAAGAGG CAGCAAGCAC AACTCGAAAT CACATGATCT TAGTTGGGAC      1050
      GGACCCCTCTA TATGGAACCTA TGTATAATCA CTACACAGGA AAGCCAATTA      1100
30     TAACAGTTCC TGGACAAAAT GTAGCAGTTA AATCCGGTAC GGCTCAAATC      1150
      GCTGATGAGA AAAATGGAGG AACTTGGTT GGTTCTACCA ATTATATTTT      1200
      CTCAGTTGTG ACTATGAATC CTGCTGAAAA TCCTGATTTT ATCTTGATG      1250
      TAACGGTTCA ACAGCCTGAG CATTATTCAG GTATCCAGTT GGGAGAATTT      1300
      GCCACCCCAA TCTTGGAGCG GGCTTCAGCT ATGAAAGAAT CTCTCAATCT      1350
35     TCAATCTCCA GCCAAAATT TAGATAAAGT TACGACAGAA TCTTCTTATG      1400
      CAATGCCTAG CATCAAGGAT ATTTACCTG GTGAGTTGGC GGAAGCCTTA      1450
      CGCCGAAATA TTGTGCAACC AATCGTTGTA GGTACTGGAA CAAAGATTAA      1500
      AGAGACTTCT GTAGAAGAAG GGACCAATCT TGCACCAAAC CAACAAGTTC      1550
      TCCTTTTATC GGATAAGGTA GAAGAAATTC CAGACATGTA TGGCTGGAAA      1600
40     AAAGAGACTG CCGAGACCTT TGCTAAATGG TTGGATATTG AACTGGAATT      1650
      TGAAGGTTCA GGTTCCTTG      1670

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2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1683 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCCCTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAAGTATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTG GTTGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACCTATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTG GTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGATGTGA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
35	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAG		1683

2) INFORMATION FOR SEQ ID NO: 1036

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-03

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTG CAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAACTC	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATTCAATGCC	TAGCATCAAG	GATATTTCAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGCACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAACTGGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1681 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGACACAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAAC TGGA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGTTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
5	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACACT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA		1685

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2) INFORMATION FOR SEQ ID NO: 1039

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1679 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTC	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTGGA	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGGTTTCAG	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAACCTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGCGGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
60	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
20	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTAACATATG	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGTTGGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCTCTATA	TGGAACATATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGTTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAGAAG	1696

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2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAAGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCTTC	AGTCCTTCAT	GGAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGTTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACCTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

60

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

5	CAAAAAAGAG	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCTAATCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGT	100
	CTAGCTCAAC	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
	TTATTACTTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
10	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTC	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
15	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCCTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
20	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
25	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
30	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
35	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG		1690

40

2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 1668 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Streptococcus pneumoniae</i>
	(B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

	AGTTGGAAAC	TGCAGAGGTC	AAGGGGATTG	ATTTTACAAC	CAGTCCTAAT	50
	CGTAGTTACC	CAAACGGACA	ATTTGCTTCT	AGTTTTATCG	GACTIONCTCA	100
60	GCTCCATGAA	AATGAAGATG	GCAGCAAGAG	CTTGCTGGGA	ACCTCTGGGA	150

	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCA	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GATAGTGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTTCG	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTCA	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAACTG	TTCCTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAAACG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGACCC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	TGAAC TGGA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTT CAGAAG			1680
25						

2) INFORMATION FOR SEQ ID NO: 1046

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTTAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCGC	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850